

**PCT**WORLD INTELLECTUAL PROPERTY ORGANIZATION  
International Bureau

## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

<b>(51) International Patent Classification <sup>6</sup> :</b> <b>C12N 15/12, 15/85, 5/10, C12Q 1/68,</b> <b>C07K 14/72, 14/685, G01N 33/566,</b> <b>A61K 38/17</b>	<b>A2</b>	<b>(11) International Publication Number: WO 98/10068</b> <b>(43) International Publication Date: 12 March 1998 (12.03.98)</b>
<b>(21) International Application Number: PCT/US97/15565</b> <b>(22) International Filing Date: 4 September 1997 (04.09.97)</b> <b>(30) Priority Data:</b> 08/706,281 4 September 1996 (04.09.96) US <b>(71) Applicant: OREGON HEALTH SCIENCES UNIVERSITY</b> [US/US]; 3181 S.W. Sam Jackson Park Road, Portland, OR 97201-3098 (US). <b>(71)(72) Applicants and Inventors:</b> CONE, Roger, D. [US/US]; 16563 S. Hattan Road, Oregon City, OR 97045 (US). FAN, Wei [CN/US]; 3323 S.W. U.S. Veterans Hospital Road, Portland, OR 97201 (US). BOSTON, Bruce, A. [US/US]; 1589 Worthington, Portland, OR 97034 (US). KESTERTON, Robert, A. [US/US]; 8326 S.E. 28th Avenue, Portland, OR 97202 (US). LU, Dongsu [CN/US]; 5181 S.W. 158th Avenue, Beaverton, OR 97007 (US). CHEN, Wenbiao [CN/US]; Apartment 6, 3415 S.W. 11th Avenue, Portland, OR 97201 (US). <b>(74) Agent: NOONAN, Kevin, E.; McDonnell Boehnen Hulbert &amp; Berghoff, 300 South Wacker Drive, Chicago, IL 60606 (US).</b>	<b>(81) Designated States:</b> AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, UZ, VN, ARIPO patent (GH, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).  <b>Published</b> <i>Without international search report and to be republished upon receipt of that report.</i>	
<b>(54) Title: METHODS AND REAGENTS FOR DISCOVERING AND USING MAMMALIAN MELANOCORTIN RECEPTOR AGONISTS AND ANTAGONISTS TO MODULATE FEEDING BEHAVIOR IN ANIMALS</b>		
<b>(57) Abstract</b> <p>The present invention provides recombinant expression constructs comprising nucleic acid encoding mammalian melanocortin receptors, and mammalian cells into which said recombinant expression constructs have been introduced that express functional mammalian melanocortin receptors. The invention provides a panel of such transformed mammalian cells expressing melanocortin receptors for screening compounds for receptor agonist and antagonist activity. The invention also provides methods for using such panels of melanocortin receptor-expressing mammalian cells to specifically detect and identify agonists and antagonists for each melanocortin receptor, as well as patterns of agonist and antagonist activity of said compounds for the class of melanocortin receptors. Such screening methods provide a means for identifying compounds with patterns of melanocortin agonist and antagonist activity which is associated with the capacity to influence or modify metabolism and behavior, particularly feeding behavior.</p>		

BEST AVAILABLE COPY

**FOR THE PURPOSES OF INFORMATION ONLY**

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece			TR	Turkey
BG	Bulgaria	HU	Hungary	ML	Mali	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MN	Mongolia	UA	Ukraine
BR	Brazil	IL	Israel	MR	Mauritania	UG	Uganda
BY	Belarus	IS	Iceland	MW	Malawi	US	United States of America
CA	Canada	IT	Italy	MX	Mexico	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NE	Niger	VN	Viet Nam
CG	Congo	KE	Kenya	NL	Netherlands	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NO	Norway	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	NZ	New Zealand		
CM	Cameroon			PL	Poland		
CN	China	KR	Republic of Korea	PT	Portugal		
CU	Cuba	KZ	Kazakstan	RO	Romania		
CZ	Czech Republic	LC	Saint Lucia	RU	Russian Federation		
DE	Germany	LI	Liechtenstein	SD	Sudan		
DK	Denmark	LK	Sri Lanka	SE	Sweden		
EE	Estonia	LR	Liberia	SG	Singapore		

**METHODS AND REAGENTS FOR DISCOVERING AND USING  
MAMMALIAN MELANOCORTIN RECEPTOR AGONISTS AND  
ANTAGONISTS TO MODULATE FEEDING BEHAVIOR IN ANIMALS**

5

**BACKGROUND OF THE INVENTION**

**1. Field of the Invention**

The present invention relates to the cloning, expression and functional characterization of mammalian melanocortin receptor genes. The invention provides nucleic acid encoding mammalian melanocortin receptors, recombinant expression constructs comprising said nucleic acid, and mammalian cells into which said recombinant expression constructs have been introduced, and that express functional mammalian melanocortin receptors. The invention also provides a panel of such transformed mammalian cells expressing melanocortin receptors for screening compounds for receptor agonist and antagonist activity. The invention provides methods for using such panels of melanocortin receptor-expressing mammalian cells to specifically detect and identify agonists and antagonists for each melanocortin receptor, as well as patterns of agonist and antagonist activity of said compounds for the class of melanocortin receptors. Such screening methods provide a means for identifying compounds with patterns of melanocortin agonist and antagonist activity which is associated with the capacity to influence or modify physiological function and behavior, particularly metabolism and feeding behavior.

**2. Background of the Invention**

The proopiomelanocortin (POMC) gene product is processed to produce a large number of biologically active peptides. Two of these peptides,  $\alpha$ -melanocyte stimulating hormone ( $\alpha$ MSH), and adrenocorticotrophic hormone (ACTH) have well understood roles in control of melanocyte and adrenocortical function, respectively. Both of these hormones are also found in a variety of forms with unknown functions, for example,  $\gamma$ -melanocyte stimulating hormone ( $\gamma$ MSH), which has little or no ability to stimulate pigmentation (Ling *et al.*, 1979, *Life Sci.* 25: 1773-1780; Slominski *et al.*, 1992, *Life Sci.* 50: 1103-1108). A melanocortin receptor gene specific for each of the  $\alpha$ MSH, ACTH and  $\gamma$ MSH hormones has been discovered by some of the present inventors (*see* U.S. Patent Nos. 5,280,112, 5,532,347 and U.S. Application Serial No. 08/044,812, incorporated by reference herein). In addition, two other melanocortin receptor genes

have been discovered by some of the present inventors (*see* Lu *et al.*, 1994, *Nature* 371: 799-802; Mountjoy *et al.*, 1994, *Molec. Endocrinol.* 8: 1298-1308) and others (*see* Gantz *et al.*, 1993, *J. Biol. Chem.* 268: 15174-15179 and Labbe *et al.*, 1994, *Biochem.* 33: 4543-4549).

5           Along with the well-recognized activities of  $\alpha$ MSH in melanocytes and ACTH in adrenal and pituitary glands, the melanocortin peptides also have a diverse array of biological activities in other tissues, including the brain and immune system, and bind to specific receptors in these tissues with a distinct pharmacology (*see*, Hanneman *et al.*, in *Peptide Hormone as Prohormones*, G. Martinez, ed. (Ellis Horwood Ltd.: Chichester, UK) pp. 53-82; DeWied & Jolles, 1982, *Physiol. Rev.* 62: 976-1059 for reviews). A  
10           complete understanding of these peptides and their diverse biological activities requires the isolation and characterization of their corresponding receptors. Some biochemical studies have been reported in the prior art.

          Shimizu, 1985, *Yale J. Biol. Med.* 58: 561-570 discusses the physiology of  
15           melanocyte stimulating hormone.

          Tatro & Reichlin, 1987, *Endocrinology* 121: 1900-1907 disclose that MSH receptors are widely distributed in rodent tissues.

          Sola *et al.*, 1989, *J. Biol. Chem.* 264: 14277-14280 disclose the molecular weight characterization of mouse and human MSH receptors linked to radioactively and  
20           photoaffinity labeled MSH analogues.

          Siegrist *et al.*, 1991, *J. Receptor Res.* 11: 323-331 disclose the quantification of receptors on mouse melanoma tissue by receptor autoradiography.

          Cone & Mountjoy, U.S. Patent No. 5,532,347 disclose the isolation of human and mouse  $\alpha$ -MSH receptor genes and uses thereof (incorporated herein by reference).

25           Cone & Mountjoy, U.S. Patent No. 5,280,112 disclose the isolation of human and bovine ACTH receptor genes and uses thereof (incorporated herein by reference).

          Mountjoy *et al.*, 1992, *Science* 257: 1248-1251 disclose the isolation of cDNAs encoding mammalian ACTH and MSH receptor proteins.

          POMC neurons are present in only two regions of the brain, the arcuate nucleus  
30           of the hypothalamus, and the nucleus of the solitary tract of the brain stem. Neurons from both sites project to a number of hypothalamic nuclei known to be important in feeding behavior, including the paraventricular nucleus, lateral hypothalamic area, and

ventromedial hypothalamic nucleus. While previous reports have claimed both stimulatory and inhibitory effects of  $\alpha$ -MSH on feeding behavior (*see Shimizu et al.*, 1989, *Life Sci.* 45: 543-552; Tsujii *et al.*, 1989, *Brian Res. Bull.* 23: 165-169), knowledge of specific melanocortin receptors, their location within the central nervous system and the necessary pharmacological tools were not sufficiently developed at that time to allow the resolution of this issue. The present inventors have shown herein that a novel antagonist of the MC-3 and MC-4 melanocortin receptors can substantially increase food consumption in animals engaged in normal or fast-induced feeding behavior. This is consistent with expression of both MC-3 and MC-4 receptor mRNAs at these sites in *in situ* hybridization studies (Roselli-Rehfuss *et al.*, 1993, *Proc. Natl. Acad. Sci. USA* 90: 8856-8860; Mountjoy *et al.*, 1994, *Molec. Endocrinol.* 8: 1298-1308). Moreover, the regulation of arcuate nucleus POMC gene expression is consistent with an inhibitory role for POMC in feeding behavior. POMC mRNA levels are decreased following a fast (Bergendahl *et al.*, 1992, *Neuroendocrinol.* 56: 913-920; Brady *et al.*, 1990, *Neuroendocrinol.* 52: 441-447), and a significant diurnal variation in POMC mRNA levels in the arcuate nucleus is seen in rat, with the nadir occurring around the onset of nighttime feeding at 1800 hrs (Steiner *et al.*, 1994, *FASEB J.* 8: 479-488).

Thus, the experimental evidence indicates that POMC neurons play an important role in tonic inhibition of feeding behavior, wherein obesity results from a chronic disruption of this inhibitory tone by antagonism of central melanocortin receptors in at least one animal model (*agouti*).

These results reveal for the first time a need in the art for a means for characterizing mammalian melanocortin receptor agonists and antagonists *in vitro* for the development of compounds that affect feeding behavior in animals.

### SUMMARY OF THE INVENTION

The present invention provides a biological screening system for identifying and characterizing compounds that are agonists or antagonists of mammalian melanocortin receptors. The biological screening system of the invention comprises a panel of transformed mammalian cells comprising a recombinant expression construct encoding

a mammalian melanocortin receptor, and expressing said receptor thereby. The invention provides such a panel of transformed mammalian cells wherein the panel comprises cells expressing each type of mammalian melanocortin receptor. Thus, the invention also provides nucleic acid encoding mammalian melanocortin receptors, recombinant expression constructs comprising said nucleic acid, and mammalian cells into which said recombinant expression constructs have been introduced, and that express functional mammalian melanocortin receptors. Methods for using such panels of melanocortin receptor-expressing mammalian cells to specifically detect and identify agonists and antagonists for each melanocortin receptor, as well as patterns of agonist and antagonist activity of said compounds for the class of melanocortin receptors, are also provided. Such screening methods provide a means for identifying compounds with patterns of melanocortin agonist and antagonist activity which is associated with the capacity to influence or modify metabolism and behavior in an animal, particularly feeding behavior.

Thus, the invention provides in a first aspect a biological screening panel for determining the melanocortin receptor agonist/antagonist profile of a test compound. The panel comprises a first mammalian cell comprising a recombinant expression construct encoding a mammalian melanocortin receptor that is the  $\alpha$ -MSH (MC-1) receptor. The panel also comprises a second mammalian cell comprising a recombinant expression construct encoding a mammalian melanocortin receptor that is the ACTH (MC-2) receptor. The panel also comprises a third mammalian cell comprising a recombinant expression construct encoding a mammalian melanocortin receptor that is the MC-3 receptor. The panel also comprises a fourth mammalian cell comprising a recombinant expression construct encoding a mammalian melanocortin receptor that is the MC-4 receptor. The panel also comprises a fifth mammalian cell comprising a recombinant expression construct encoding a mammalian melanocortin receptor that is the MC-5 receptor. As provided by the invention, each mammalian cell expresses the melanocortin receptor encoded by the recombinant expression construct comprising said cell.

In preferred embodiments, the melanocortin receptors encoded by the recombinant expression constructs comprising the transformed mammalian cells comprising the panel are mouse MC-1 receptor (SEQ ID Nos.: 3 and 4); human MC-1

receptor (SEQ ID Nos.: 5 and 6), human MC-2 (ACTH) receptor (SEQ ID Nos.: 7 and 8), bovine MC-2 receptor (SEQ ID Nos.: 9 and 10), rat MC-3 receptor (SEQ ID Nos.: 11 and 12), human MC-4 receptor (SEQ ID Nos.: 15 and 16) and mouse MC-5 receptor (SEQ ID Nos.: 17 and 18).

5           In a second aspect, the invention provides a method for using the melanocortin receptor panel to identify and characterize test compounds as melanocortin receptor agonists and/or antagonists. In this embodiment, the method provided by the invention identifies a melanocortin receptor agonist, and comprises the steps of contacting each of the cells of the panel with a test compound to be characterized as an agonist of a  
10           mammalian melanocortin receptor and detecting binding of the test compound to each of the mammalian melanocortin receptors by assaying for a metabolite produced in the cells that bind the compound. In a preferred embodiment, the detected metabolite is cAMP.

          In a preferred embodiment of this method, each of the cells of the panel of  
15           mammalian cells expressing mammalian melanocortin receptors further comprises a recombinant expression construct encoding a cyclic AMP responsive element (CRE) transcription factor binding site that is operatively linked to a nucleic acid sequence encoding a protein capable of producing a detectable metabolite. In preferred  
20           embodiments, said protein is  $\beta$ -galactosidase, most preferably encoded by a nucleic acid comprising the recombinant expression construct identified as pCRE/ $\beta$ -galactosidase (as disclosed in Chen *et al.*, 1994, *Analyt. Biochem.* 226: 349-354). As provided by the invention, expression of the protein that produces the detectable metabolite is dependent on binding of the test compound to the melanocortin receptor expressed by each cell in the panel and the intracellular production of cAMP as a result. In this embodiment,  
25           cAMP production results in expression of a protein capable of producing a detectable metabolite, the protein most preferably being  $\beta$ -galactosidase. In preferred embodiments, the detectable metabolite absorbs light to produce a colored product. Thus, this embodiment of the invention provides a panel of melanocortin receptor-expressing cells whereby melanocortin hormone binding results in the production of a  
30           colored product in proportion to the extent of cAMP production in the cell as a result of hormone receptor binding.

In another embodiment of this aspect of the invention is provided a method for characterizing a compound as an antagonist of a mammalian melanocortin receptor. In this embodiment, the method comprises the steps of contacting each of the cells of the panel with an agonist of the mammalian melanocortin receptor in an amount sufficient to produce a detectable amount of a metabolite produced in the cells that bind the agonist, in the presence or absence of a test compound to be characterized as an antagonist of a mammalian melanocortin receptor, and detecting the amount of the metabolite produced in each cell in the panel in the presence of the test compound with the amount of the metabolite produced in each cell in the panel in the absence of the test compound. As provided by the assay, inhibition of the production of the detectable metabolite is used as an indication that the tested compound is a melanocortin receptor antagonist, which is further characterized quantitatively by the extent of said inhibition.

In a preferred embodiment of this method, each of the cells of the panel of mammalian cells expressing mammalian melanocortin receptors further comprises a recombinant expression construct encoding a cyclic AMP responsive element (CRE) transcription factor binding site that is operatively linked to a nucleic acid sequence encoding a protein capable of producing a detectable metabolite. In preferred embodiments, said protein is  $\beta$ -galactosidase, most preferably encoded by a nucleic acid comprising the recombinant expression construct identified as pCRE/ $\beta$ -galactosidase. As provided by the invention, expression of the protein that produces the detectable metabolite is dependent on binding of the test compound to the melanocortin receptor expressed by each cell in the panel. In preferred embodiments, the detectable metabolite absorbs light to produce a colored product. Thus, this embodiment of the invention provides a panel of melanocortin receptor-expressing cells whereby melanocortin hormone binding results in the production of a colored product in proportion to the extent of cAMP production in the cell as a result of hormone receptor binding.

The invention also provides melanocortin receptor agonists identified by the methods and using the screening panel of the invention. In preferred embodiments, the agonist is an agonist of the MC-3 mammalian melanocortin receptor. In other preferred embodiments, the agonist is an agonist of the MC-4 mammalian melanocortin receptor.

The invention provides melanocortin receptor antagonists identified by the methods and using the screening panel of the invention. In preferred embodiments, the



antagonist is an antagonist of the MC-3 mammalian melanocortin receptor. In other preferred embodiments, the antagonist is an antagonist of the MC-4 mammalian melanocortin receptor.

5 The invention also provides methods for characterizing mammalian melanocortin receptor agonists for the capacity to modify or influence metabolism and feeding behavior in an animal. In a first aspect, the invention provides a method for characterizing melanocortin receptor MC-3 or MC-4 agonists as inhibitors of feeding behavior in an animal, the method comprising the steps of providing food to an animal that has been deprived of food for at least 12 hours, with or without administering to the animal an MC-3 or MC-4 receptor agonist of the invention, and comparing the amount of food eaten by the animal after administration of the MC-3 or MC-4 receptor agonist with the amount of food eaten by the animal without administration of the MC-3 or MC-4 receptor agonist.

15 In another aspect, the invention provides a method for characterizing a melanocortin MC-3 or MC-4 receptor antagonist as a stimulator of feeding behavior in an animal. In this embodiment, the method comprises the steps of providing food to an animal not deprived of food for at least 12 hours, with or without administering to the animal an MC-3 or MC-4 receptor antagonist, immediately prior to the onset of darkness or nighttime, and comparing the amount of food eaten by the animal after administration of the MC-3 or MC-4 receptor antagonist with the amount of food eaten by the animal without administration of the MC-3 or MC-4 receptor antagonist.

20 Thus, the invention also provides methods for using certain of the melanocortin receptor agonists and antagonists for modifying feeding behavior in an animal. In a first aspect, the invention provides a method for stimulating feeding in an animal, the method comprising administering to the animal an MC-3 or MC-4 receptor antagonist. In a preferred embodiment, the antagonists are administered systemically. In additional embodiments, the antagonists are administered intracerebroventricularly.

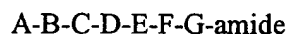
25 In another aspect, the invention provides a method for inhibiting feeding in an animal, the method comprising administering to the animal an MC-3 or MC-4 receptor agonist. In a preferred embodiment, the agonists are administered systemically. In additional embodiments, the agonists are administered intracerebroventricularly.

In yet another aspect, the invention provides mammalian melanocortin receptor agonists having the general formula:



wherein A is an aliphatic amino acid residue, including for example Leu, Ile, Nle and Met, as well as analogues and substituted derivatives thereof; B is an acidic amino acid residue, including for example Asp and Glu; C is a basic amino acid residue, such as His; D is an aromatic amino acid residue having a D- conformation, including D-Phe, D-Tyr and substituted derivatives thereof; E is a basic amino acid residue, for example Arg, Lys, homoArg, homoLys, and analogues or substituted derivatives thereof; F is Trp or substituted derivatives thereof; and G is Lys, homoLys or a substituted derivative thereof. In the peptide embodiments of the melanocortin receptor agonists of the invention, the peptide is cyclized by the formation of an amide bond between the side chain carboxyl group of the Asp or Glu residue at position B in the peptide, and the side chain amino group of the Lys or homoLys residue at position G. In preferred embodiments, the melanocortin receptor agonists of the invention are agonists of the MC-3 or MC-4 receptor.

The invention also provides mammalian melanocortin receptor antagonists having the general formula:



wherein A is an aliphatic amino acid residue, including for example Leu, Ile, Nle and Met, as well as analogues and substituted derivatives thereof; B is an acidic amino acid residue, including for example Asp and Glu; C is a basic amino acid residue, such as His; D is an aromatic amino acid residue having a D- conformation, including D-Nal and substituted derivatives thereof; E is a basic amino acid residue, for example Arg, Lys, homoArg, homoLys, and analogues or substituted derivatives thereof; F is Trp or substituted derivatives thereof; and G is Lys, homoLys or a substituted derivative thereof. In the peptide embodiments of the melanocortin receptor antagonists of the invention, the peptide is cyclized by the formation of an amide bond between the side chain carboxyl group of the Asp or Glu residue at position B in the peptide, and the side chain amino group of the Lys or homoLys residue at position G. In preferred embodiments, the melanocortin receptor antagonists of the invention are agonists of the MC-3 or MC-4 receptor.

It is an advantage of the present invention that it provides an *in vitro* screening method for characterizing compounds having melanocortin receptor activities that relate to feeding behavior in animals. Specifically, the invention advantageously provides means and methods for identifying compounds having melanocortin receptor agonist and/or antagonist activity that have been associated with either stimulating or inhibiting feeding behavior when administered to an animal. The invention thus provides an economical first step in screening compounds for the capacity to affect feeding behavior, including synthetic, peptidomimetic or organomimetic derivatives of melanocortin receptor agonists or antagonists as disclosed herein or elsewhere.

Specific preferred embodiments of the present invention will become evident from the following more detailed description of certain preferred embodiments and the claims.

#### DESCRIPTION OF THE DRAWINGS

Figures 1A and 1B illustrate the nucleotide (SEQ ID No.: 3) and amino acid (SEQ ID No.: 4) sequence of the mouse melanocyte stimulating hormone receptor gene.

Figures 2A and 2B illustrate the nucleotide (SEQ ID No.: 5) and amino acid (SEQ ID No.: 6) sequence of the human melanocyte stimulating hormone receptor gene.

Figures 3A and 3B illustrate the nucleotide (SEQ ID No.: 7) and amino acid (SEQ ID No.: 8) sequence of the human adrenocorticotrophic stimulating hormone receptor gene.

Figures 4A and 4B illustrate the nucleotide (SEQ ID No.: 9) and amino acid (SEQ ID No.: 10) sequence of the bovine adrenocorticotrophic stimulating hormone receptor gene.

Figures 5A and 5B illustrate the nucleotide (SEQ ID No.: 11) and amino acid (SEQ ID No.: 12) sequence of the rat melanocortin-3 receptor gene.

Figures 6A and 6B illustrate the nucleotide (SEQ ID No.: 15) and amino acid (SEQ ID No.: 16) sequence of the human melanocortin-4 receptor gene.

Figures 7A and 7B illustrate the nucleotide (SEQ ID No.: 17) and amino acid (SEQ ID No.: 18) sequence of the mouse melanocortin-5 receptor gene.

Figure 8 shows a graph of intracellular cAMP accumulation resulting from melanocyte stimulating hormone receptor agonist binding in human 293 cells transfected with a MSH receptor-encoding recombinant expression construct, wherein  $\square$ - represents binding of NDP-MSH,  $\circ$ - represents binding of ACTH and  $\Delta$ - represents binding of  $\alpha$ MSH.

Figure 9 illustrates the cAMP response of mouse Y1 cells to binding of melanocortin peptides to human melanocortin-2 (ACTH) receptor, as measured by the  $\beta$ -galactosidase assay described in Example 4, wherein  $\blacksquare$ - represents binding to wild-type ACTH-R and  $\blacktriangle$ - represents binding to an ACTH-R variant.

Figure 10 illustrates the results of competition binding experiments of melanocortin peptides to cells expressing a recombinant expression construct encoding the rat melanocortin-3 receptor, wherein  $\blacksquare$ - represents binding of NDP-MSH,  $\blacktriangle$ - represents binding of  $\gamma$ MSH,  $\bullet$ - represents binding of  $\alpha$ MSH,  $\circ$ - represents binding of ACTH<sub>4-10</sub> and  $\square$ - represents binding of ORG2766.

Figures 11A through 11C illustrate the results of experiments showing intracellular cAMP accumulation caused by receptor-ligand binding in human 293 cells expressing the MC-3 receptor. In Figure 11A,  $\bullet$ - represents binding of  $\alpha$ MSH,  $\blacksquare$ - represents binding of  $\gamma_2$ -MSH,  $\blacktriangle$ - represents binding of des-acetyl  $\alpha$ MSH and  $\square$ - represents binding of ACTH<sub>1-39</sub>. In Figure 11B,  $\bullet$ - represents binding of  $\gamma_1$ -MSH,  $\blacksquare$ - represents binding of  $\gamma_2$ -MSH and  $\blacktriangle$ - represents binding of des-acetyl  $\gamma$ -MSH. In Figure 11C,  $\bullet$ - represents binding of ACTH<sub>4-10</sub>,  $\blacksquare$ - represents binding of NDP-MSH and  $\blacktriangle$ - represents binding of ORG2766.

Figure 12 shows a graph of intracellular cAMP accumulation resulting from peptide binding to human melanocortin-4 receptor agonist in human 293 cells transfected with a MC-4 receptor-encoding recombinant expression construct, wherein  $\square$ - represents binding of ACTH<sub>4-10</sub>,  $\bullet$ - represents binding of ACTH<sub>1-39</sub>,  $\blacksquare$ - represents binding of NDP-MSH,  $\circ$ - represents binding of  $\alpha$ MSH,  $\Delta$ - represents binding of  $\gamma_2$ -MSH, and  $\blacktriangle$ - represents binding of des-acetyl  $\alpha$ MSH.

Figure 13 illustrates the results of cAMP accumulation and cAMP-dependent  $\beta$ -galactosidase assays of melanocortin peptide binding to a rat melanocortin-5 receptor, wherein  $\square$ - represents binding of  $\alpha$ MSH,  $\Delta$ - represents binding of  $\beta$ -MSH, and  $\circ$ -

represents binding of  $\gamma$ -MSH, each determined using the  $\beta$ -gal method, and wherein  $\blacksquare$ - represents binding of  $\alpha$ MSH,  $\blacktriangle$ - represents binding of  $\beta$ -MSH, and  $\bullet$ - represents binding of  $\gamma$ -MSH, each determined using the cAMP method.

Figure 14 illustrates the structure of the pCRE/  $\beta$ -gal plasmid.

5           Figure 15 illustrates the results of the  $\beta$ -galactosidase-coupled, colorimetric melanocortin receptor binding assay using cells expressing each of the MC- 1, MC-3, MC4 or MC-5 receptors and contacted with  $\alpha$ MSH or a variety of  $\alpha$ MSH analogues, wherein  $\blacksquare$ - represents binding of  $\alpha$ MSH,  $\blacktriangle$ - represents binding of NDP-MSH,  $\bullet$ - represents binding of SHU9128 (*para*-F1 substituted),  $\square$ - represents binding of SHU9203 (*p*-Cl substituted),  $\Delta$ - represents binding of SHU8914 (*p*-I substituted), and  $\circ$ - represents binding of SHU9119.

          Figures 16A through 16 D show the results of the  $\beta$ -galactosidase-coupled, colorimetric melanocortin receptor binding assay to determine antagonist activity of melanocortin analogues SHU9119 and SHU8914 in cells expressing each of the melanocortin receptors MC-3 and MC-4. In Figure 16A,  $\blacksquare$ - represents binding of  $\alpha$ MSH,  $\square$ - represents binding of 100nM SHU9119,  $\Delta$ - represents binding of 10nM SHU9119, and  $\circ$ - represents binding of 1nM SHU9119. In Figure 16B,  $\blacksquare$ - represents binding of  $\alpha$ MSH,  $\square$ - represents binding of 100nM SHU9119,  $\Delta$ - represents binding of 50nM SHU9119, and  $\circ$ - represents binding of 10nM SHU9119. In Figure 16C,  $\blacksquare$ - represents binding of  $\alpha$ MSH,  $\square$ - represents binding of 1000nM SHU8914,  $\Delta$ - represents binding of 100nM SHU8914, and  $\circ$ - represents binding of 10nM SHU8614. In Figure 16D,  $\blacksquare$ - represents binding of  $\alpha$ MSH,  $\square$ - represents binding of 100nM SHU8914,  $\Delta$ - represents binding of 50nM SHU8914, and  $\circ$ - represents binding of 10nM SHU8614.

25           Figure 17 shows the results of classic competition binding assays using the melanocortin analogues SHU9119 and SHU8914 at the MC3-R and MC-4 R receptors, wherein  $\blacksquare$ - represents binding of NDP-MSH,  $\Delta$ - represents binding of SHU8914 (*p*-I substituted), and  $\circ$ - represents binding of SHU9119.

30           Figures 18A and 18B shows the results of cAMP accumulation experiments (performed using the  $\beta$ -galactosidase assay of Example 4) for rat MC-3 receptor (Figure 18A) and for mouse MC-4 receptor (Figure 18B). In Figure 18A,  $\blacksquare$ - represents

binding of NDP-MSH, -▲- represents binding of MTII and -▼- represents binding of forskolin. In Figure 18B, -■- represents binding of MTII, -▲- represents binding of NDP-MSH and -▼- represents binding of forskolin.

5        Figures 19A through 19C show the effect on food intake of intracerebroventricular administration of melanocortin analogue SHU9119 in mice. In Figure 19A, -■- represents administration of acsf (n=7) and -●- represents administration of 6nmol of SHU9119 (n=6). In Figure 19B, -■- represents administration of acsf (n=6) and -□- represents administration of 6nmol of SHU9119 (n=6). In Figure 19C, -○- represents administration of acsf (n=11) and -●- represents administration of 6nmol of SHU9119 (n=12).  
10

      Figures 20A through 20C show the effect on food intake of intracerebroventricular administration of melanocortin analogue MTII in mice. In Figure 20A, -●- represents administration of acsf (n=8), -▼- represents administration of 0.1nmol MTII (n=8), -■- represents administration of 1nmol MTII (n=7) and -▲- represents administration of 3nmol MTII (n=9). In Figure 20B, -●- represents administration of acsf (n=12), -□- represents administration of 3nmol MTII and 6nmol SHU9119 (n=9) and -▲- represents administration of 3nmol MTII (n=9).  
15

      Figure 20D shows the effect on locomotor activity of intracerebroventricular administration of melanocortin analogue MTII in mice, wherein -■- represents administration of vehicle alone (n=6) and -▲- represents administration of 3nmol MTII (n=6).  
20

      Figures 21A through 21D show the effect on food intake of intracerebroventricular administration of melanocortin analogue MTII in mice. In Figure 21A, -●- represents administration of acsf (n=6) and -▲- represents administration of 3nmol MTII (n=7). In Figure 21B, open bars represent administration of acsf (n=6), solid bars represents administration of 1.18nmol neuropeptide Y (NPY; n=6) and stipled bars represents administration of 3nmol MTII and 1.18nmol NPY (n=6). In Figure 21C, -●- represents administration of acsf (n=7) and -▲- represents administration of 3nmol MTII (n=7). In Figure 21D, -■- represents administration of 100nmol MTII (n=6) and -▲- represents administration of vehicle alone (n=6).  
25  
30

### DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

The term "melanocortin receptor" as used herein reference to proteins having the biological activity of any of the disclosed melanocortin receptors, including the MC-1 (SEQ ID Nos.: 3, 4, 5 and 6), MC-2 (ACTH; SEQ ID Nos.: 7, 8, 9 and 10), MC-3 (SEQ ID Nos.: 11 and 12), MC-4 (SEQ ID Nos.: 15 and 16) or MC-5 (SEQ ID Nos.: 17 and 18) receptors, as well as naturally-occurring and genetically-engineered allelic variations in these sequences.

Cloned nucleic acid provided by the present invention may encode MC receptor protein of any species of origin, including, for example, mouse, rat, rabbit, cat, and human, but preferably the nucleic acid provided by the invention encodes MC receptors of mammalian, most preferably rodent and human, origin.

The production of proteins such as the MC receptors from cloned genes by genetic engineering means is well known in this art. The discussion which follows is accordingly intended as an overview of this field, and is not intended to reflect the full state of the art.

DNA which encodes MC receptors may be obtained, in view of the instant disclosure, by chemical synthesis, by screening reverse transcripts of mRNA from appropriate cells or cell line cultures, by screening genomic libraries from appropriate cells, or by combinations of these procedures, as illustrated below. Screening of mRNA or genomic DNA may be carried out with oligonucleotide probes generated from the MC receptor gene sequence information provided herein. Probes may be labeled with a detectable group such as a fluorescent group, a radioactive atom or a chemiluminescent group in accordance with know procedures and used in conventional hybridization assays, as described in greater detail in the Examples below. In the alternative, MC receptor gene sequences may be obtained by use of the polymerase chain reaction (PCR) procedure, with the PCR oligonucleotide primers being produced from the MC receptor gene sequences provided herein. *See* U.S. Patent Nos. 4,683,195 to Mullis *et al.* and 4,683,202 to Mullis.

MC receptor proteins may be synthesized in host cells transformed with a recombinant expression construct comprising a nucleic acid encoding each of the receptors disclosed herein. Such a recombinant expression construct can also be comprised of a vector that is a replicable DNA construct. Vectors are used herein either

to amplify DNA encoding an MC receptor and/or to express DNA which encodes an MC receptor. For the purposes of this invention, a recombinant expression construct is a replicable DNA construct in which a DNA sequence encoding an MC receptor is operably linked to suitable control sequences capable of effecting the expression of the receptor in a suitable host cell. The need for such control sequences will vary depending upon the host selected and the transformation method chosen. Generally, control sequences include a transcriptional promoter, an optional operator sequence to control transcription, a sequence encoding suitable mRNA ribosomal binding sites, and sequences which control the termination of transcription and translation. Amplification vectors do not require expression control domains. All that is needed is the ability to replicate in a host, usually conferred by an origin of replication, and a selection gene to facilitate recognition of transformants. *See, Sambrook et al., 1990, Molecular Cloning: A Laboratory Manual* (Cold Spring Harbor Press: New York).

Also specifically provided by the invention are reporter expression constructs comprising a nucleic acid encoding a protein capable of expressing a detectable phenotype, such as the production of a detectable reporter molecule, in a cell expressing the construct. Such constructs can be used for producing recombinant mammalian cell lines in which the reporter construct is stably expressed. Most preferably, however, the reporter construct is provided and used to induce transient expression over an experimental period of from about 18 to 96 hrs in which detection of the reporter protein-produced detectable metabolite comprises an assay. Such reporter expression constructs are also provided wherein induction of expression of the reporter construct is controlled by a responsive element operatively linked to the coding sequence of the reporter protein, so that expression is induced only upon proper stimulation of the responsive element. Exemplary of such a responsive element is a cAMP responsive element (CRE), which induces expression of the reporter protein as a result of an increase in intracellular cAMP concentration. In the context of the present invention, such a stimulus is associated with melanocortin receptor binding, so that a reporter construct comprising one or more CREs is induced to express the reporter protein upon binding of a receptor agonist to a MC receptor in a recombinantly transformed mammalian cell. Production and use of such a reporter construct is illustrated below in Example 5.



Vectors useful for practicing the present invention include plasmids, viruses (including phage), retroviruses, and integratable DNA fragments (*i.e.*, fragments integratable into the host genome by homologous recombination). The vector replicates and functions independently of the host genome, or may, in some instances, integrate into the genome itself. Suitable vectors will contain replicon and control sequences which are derived from species compatible with the intended expression host. A preferred vector is the plasmid pcDNA/neo I. Transformed host cells are cells which have been transformed or transfected with recombinant expression constructs made using recombinant DNA techniques and comprising mammalian MC receptor-encoding sequences. Preferred host cells are human 293 cells. Preferred host cells for the MC-2 (ACTH) receptor are Y1 cells (subclone OS3 or Y6). Transformed host cells are chosen that ordinarily express functional MC receptor protein introduced using the recombinant expression construct. When expressed, the mammalian MC receptor protein will typically be located in the host cell membrane. *See, Sambrook et al., ibid.*

Cultures of cells derived from multicellular organisms are a desirable host for recombinant MC receptor protein synthesis. In principal, any higher eukaryotic cell culture is workable, whether from vertebrate or invertebrate culture. However, mammalian cells are preferred, as illustrated in the Examples. Propagation of such cells in cell culture has become a routine procedure. *See Tissue Culture*, Academic Press, Kruse & Patterson, editors (1973). Examples of useful host cell lines are human 293 cells, VERO and HeLa cells, Chinese hamster ovary (CHO) cell lines, mouse Y1 (subclone OS3), and WI138, BHK, COS-7, CV, and MDCK cell lines. Human 293 cells are preferred.

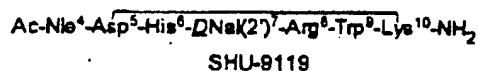
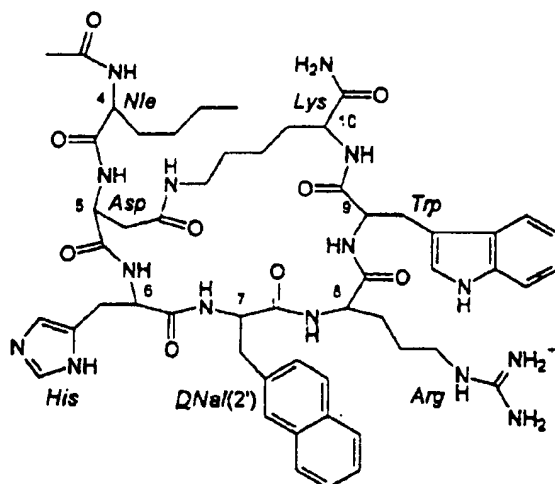
Cells expressing mammalian MC receptor proteins made from cloned genes in accordance with the present invention may be used for screening agonist and antagonist compounds for MC receptor activity. Competitive binding assays are well known in the art and are described in the Examples below. Such assays are useful for drug screening of MC receptor agonist and antagonist compounds, as detected in receptor binding assays as described below.

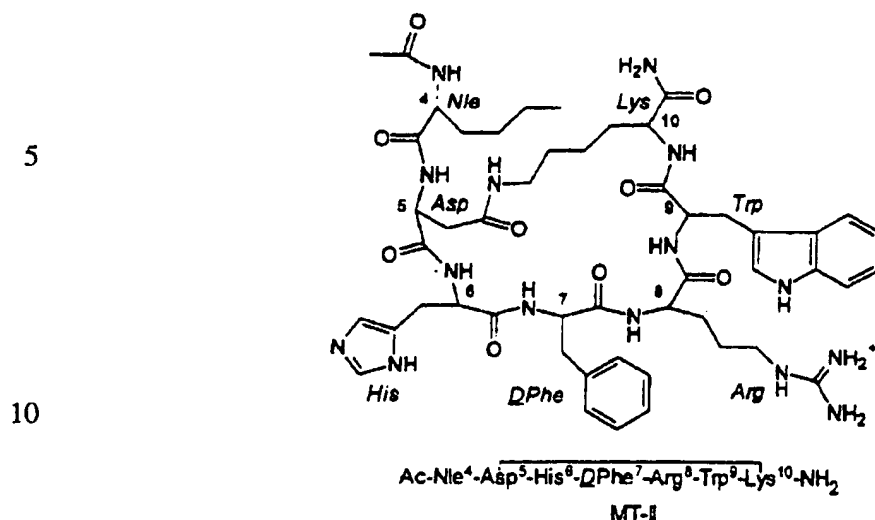
One particular use of such screening assays are for developing drugs and other compounds useful in modifying or changing feeding behavior in mammals. The invention provides an assay system, comprising a panel of recombinant mammalian

cells, heterologously expressing each of the MC receptors disclosed herein, wherein the panel is constructed of at least one cell line expressing an MC receptor, and most preferably comprising cells expressing each of the MC receptors. The invention provides such panels also comprising a detection means for detecting receptor agonist or antagonist binding, such as the reporter expression constructs described herein, using direct binding and competition binding assays as described in the Examples below. In the use of this panel, each MC receptor is assayed for agonist or antagonist patterns of binding a test compound, and a characteristic pattern of binding for all MC receptors is thereby determined for each test compound. This pattern is then compared with known MC receptor agonists and antagonists to identify new compounds having a pattern of receptor binding activity associated with a particular behavioral or physiological effect.

For example, provided herein is experimental evidence that MC-3 or MC-4 receptor antagonists are capable of stimulating feeding in hungry animals, and that MC-3 or MC-4 agonists are capable of inhibiting feeding in animals otherwise stimulated to eat. The invention provides an *in vitro* assay to characterize MC-3 and MC-4 agonists/antagonists as a preliminary and economical step towards developing feeding behavior-modulating drugs for use *in vivo*.

These results on feeding behavior *in vivo* have been obtained with certain MC receptor binding analogues, SHU9119 and MTII. These compounds have the following chemical structure:





15 Generally, those skilled in the art will recognize that peptides as described herein may be modified by a variety of chemical techniques to produce compounds having essentially the same activity as the unmodified peptide, and optionally having other desirable properties. For example, carboxylic acid groups of the peptide, whether carboxyl-terminal or sidechain, may be provided in the form of a salt of a pharmaceutically-acceptable cation or esterified to form a C<sub>1</sub>-C<sub>16</sub> ester, or converted

20 to an amide of formula NR<sub>1</sub>R<sub>2</sub> wherein R<sub>1</sub> and R<sub>2</sub> are each independently H or C<sub>1</sub>-C<sub>16</sub> alkyl, or combined to form a heterocyclic ring, such as 5- or 6-membered. Amino groups of the peptide, whether amino-terminal or sidechain, may be in the form of a pharmaceutically-acceptable acid addition salt, such as the HCl, HBr, acetic, benzoic, toluene sulfonic, maleic, tartaric and other organic salts, or may be modified to C<sub>1</sub>-C<sub>16</sub>

25 alkyl or dialkyl amino or further converted to an amide. Hydroxyl groups of the peptide sidechain may be converted to C<sub>1</sub>-C<sub>16</sub> alkoxy or to a C<sub>1</sub>-C<sub>16</sub> ester using well-recognized techniques. Phenyl and phenolic rings of the peptide sidechain may be substituted with one or more halogen atoms, such as fluorine, chlorine, bromine or iodine, or with C<sub>1</sub>-C<sub>16</sub> alkyl, C<sub>1</sub>-C<sub>16</sub> alkoxy, carboxylic acids and esters thereof, or amides of such carboxylic acids. Methylene groups of the peptide sidechains can be

30 extended to homologous C<sub>2</sub>-C<sub>4</sub> alkylenes. Thiols can be protected with any one of a

number of well-recognized protecting groups, such as acetamide groups. Those skilled in the art will also recognize methods for introducing cyclic structures into the peptides of this invention to select and provide conformational constraints to the structure that result in enhanced binding and/or stability. For example, a carboxyl-terminal or amino-terminal cysteine residue can be added to the peptide, so that when oxidized the peptide will contain a disulfide bond, thereby generating a cyclic peptide. Other peptide cyclizing methods include the formation of thioethers and carboxyl- and amino-terminal amides and esters.

Peptidomimetic and organomimetic embodiments are also hereby explicitly declared to be within the scope of the present invention, whereby the three-dimensional arrangement of the chemical constituents of such peptido- and organomimetics mimic the three-dimensional arrangement of the peptide backbone and component amino acid sidechains in the peptide, resulting in such peptido- and organomimetics of the peptides of this invention having substantial biological activity. It is implied that a pharmacophore exists for the receptor agonist and antagonist properties of these and related MC receptor binding analogues. A pharmacophore is an idealized, three-dimensional definition of the structural requirements for biological activity. Peptido- and organomimetics can be designed to fit each pharmacophore with current computer modeling software (computer aided drug design). MC receptor binding analogues derived using such software and comprising peptido- and organomimetics of SHU9119 and MTII and related analogues are within the scope of the claimed invention.

The MC receptor binding analogues, in particular those analogues that are MC-3 or MC-4 receptor agonists or antagonists are provided to be used in methods of influencing, modifying or changing feeding behavior in mammals *in vivo*. Specific examples of uses for the MC receptor binding analogues of the invention include but are not limited to treatment of eating disorders such as anorexia and obesity, and other pathological weight and eating-related disorders. Other examples are failure to thrive disorders and disease-related cachexia, such as occurs in cancer patients. Also within the scope of the analogues of the invention is use for enhancing appearance, athletic ability, or adjuvant to other therapies to treat disorders such as high blood pressure, high

serum cholesterol, vascular and heart disease, stroke, kidney disease, diabetes and other metabolic disorders.

The Examples which follow are illustrative of specific embodiments of the invention, and various uses thereof. They set forth for explanatory purposes only, and are not to be taken as limiting the invention.

#### EXAMPLE 1

##### Isolation of an $\alpha$ MSH Receptor Probe by Random PCR Amplification of Human Melanoma cDNA Using Degenerate Oligonucleotide Primers

In order to clone novel G-protein coupled receptors, cDNA prepared from RNA from human melanoma cells was used as template for a polymerase chain reaction (PCR)-based random cloning experiment. PCR was performed using a pair of degenerate oligonucleotide primers corresponding to the putative third and sixth transmembrane regions of G-protein coupled receptors (Libert *et al.*, 1989, *Science* 244: 569-72; Zhou *et al.*, 1990, *Nature* 347: 76-80). The PCR products obtained in this experiment were characterized by nucleotide sequencing. Two novel sequences representing novel G-protein-coupled receptors were identified.

PCR amplification was performed as follows. Total RNA was isolated from a human melanoma tumor sample by the guanidinium thiocyanate method (Chirgwin *et al.*, 1979, *Biochemistry* 18: 5294-5299). Double-stranded cDNA was synthesized from total RNA with murine reverse transcriptase (BRL, Gaithersburg, MD) by oligo-dT priming (Sambrook *et al.*, *ibid.*). The melanoma cDNA mixture was then subjected to 45 cycles of PCR amplification using 500 picomoles of degenerate oligonucleotide primers having the following sequence:

Primer III (sense):

GAGTCGACCTGTG(C/T)G(C/T)(C/G)AT(C/T)(A/G)CIIT(G/T)GAC(C/A)G(C/G)TAC  
(SEQ ID NO:1)

and

Primer VI (antisense):

CAGAATTTCAG(T/A)AGGGCAICCCAGCAGAI(G/C)(G/A)(T/C)GAA  
(SEQ ID NO:2)

in 100  $\mu$ l of a solution containing 50 mM Tris-HCl (pH 8.3), 2.5 mM  $MgCl_2$ , 0.01% gelatin, 200  $\mu$ M each dNTP, and 2.5 units of *Taq* polymerase (Saiki *et al.*, 1988, *Science* 239: 487-491). These primers were commercially synthesized by Research Genetics Inc. (Huntsville, AL). Each PCR amplification cycle consisted of incubations  
5 at 94°C for 1 min (denaturation), 45 C for 2 min (annealing), and 72 C for 2 min (extension).

Amplified products of the PCR reaction were extracted with phenol/chloroform and precipitated with ethanol. After digestion with *Eco*RI and *Sal*I, the PCR products were separated on a 1.2% agarose gel. A slice of this gel, corresponding to PCR  
10 products of 300 basepairs (bp) in size, was cut out and purified using glass beads and sodium iodide, and the insert was then cloned into a pBKS cloning vector (Stratagene, LaJolla, CA).

A total of 172 of such pBKS clones containing inserts were sequenced using Sequenase (U.S. Biochemical Corp., Cleveland, OH) by the dideoxynucleotide chain  
15 termination method (Sanger *et al.*, 1977, *Proc. Natl. Acad. Sci. USA* 74: 5463-5467). Two types of sequences homologous to other G-protein coupled receptors were identified.

## EXAMPLE 2A

### 20 Isolation of a Mouse $\alpha$ MSH (MC-1) Receptor cDNA

Probes isolated in Example 1 was used to screen a Cloudman melanoma cDNA library in order to isolate a full-length cDNA corresponding to the cloned probe. One clone was isolated from a library of  $5 \times 10^6$  clones screened as described below in Example 2B. This clone contained an insert of 2.6 kilobases (kb). The nucleotide  
25 sequence of the complete coding region was determined (*see* co-owned U.S. Patent No. 5,532,347, incorporated by reference); a portion of this cDNA comprising the coding region was sequenced and is shown in Figures 1A and 1B (SEQ ID Nos: 3 & 4).

## EXAMPLE 2B

### 30 Isolation of a Human $\alpha$ MSH (MC-1) Receptor cDNA

In order to isolate a human counterpart of the murine melanocyte  $\alpha$ MSH receptor gene disclosed in Example 2A and co-owned U.S. Patent No. 5,532,347, a

human genomic library was screened at high stringency (50% formamide, 42°C) using the human PCR fragments isolated as described in Example 1. A genomic clone was determined to encode an human MSH receptor (SEQ ID NO:5). The human MSH receptor has a predicted amino acid sequence (SEQ ID NO:6) that is 75% identical and colinear with the mouse  $\alpha$ MSH receptor cDNA sequence (Figures 2A and 2B, represented as human MSH-R). The predicted molecular weight of the human MSH<sup>R</sup> is 34.7kD.

## EXAMPLE 2C

### Isolation of a Human ACTH (MC-2) Receptor cDNA

For cloning the ACTH receptor (MC-2), a human genomic library was screened at high stringency (50% formamide, 1M NaCl, 50nM Tris-HCl, pH 7.5, 0.1% sodium pyrophosphate, 0.2% sodium dodecyl sulfate, 100 $\mu$ g/ml salmon sperm DNA, 10X Denhardt's solution, 42°C), using the human PCR fragments isolated as described in Example 1 herein and U.S. Patent No. 5,280,112, incorporated by reference. A genomic clone was isolated that encodes a highly related G-coupled receptor protein (SEQ ID NO:7 and Figures 3A and 3B). The predicted amino acid sequence (SEQ ID NO:8) of this clone is 39% identical and also colinear, excluding the third intracellular loop and carboxy-terminal tail, with the human MSH receptor gene product.' The predicted molecular weight of this putative ACTH<sup>R</sup> is 33.9 kilodaltons (kD). This clone was identified as encoding an MC-2 receptor based on its high degree of homology to the murine and human MSH receptors, and the pattern of expression in different tissue types, as described in Example 3 in U.S. Patent 5,280,112.

## EXAMPLE 2D

### Isolation of a Bovine ACTH (MC-2) Receptor cDNA

A bovine genomic DNA clone encoding the bovine counterpart of the MC-2 (ACTH) receptor was isolated from a bovine genomic library, essentially as described in Example 2C above, and its nucleotide sequence determined (as shown in Figures 4A and 4B; SEQ ID Nos:9 & 10).

**EXAMPLE 2E****Isolation of a Rat  $\gamma$ -MSH (MC-3) Receptor cDNA**

The mouse  $\alpha$ MSH receptor cDNA isolated as described in Example 2A and co-owned U.S. Patent No. 5,532,347 was used to screen a rat hypothalamus cDNA library at low stringency (30% formamide, 5X SSC, 0.1% sodium pyrophosphate, 0.2% sodium dodecyl sulfate, 100 $\mu$ g/ml salmon sperm DNA, and 10% Denhardt's solution) at 42°C for 18h. A 1 kb cDNA clone was isolated and sequenced as described in co-owned U.S. Patent No. 5,532,347, and this clone used to re-screen the rat hypothalamus cDNA library at high stringency (same conditions as above except that formamide was present at 45%). A cDNA clone approximately 2.0 kb in length was isolated and analyzed as described in co-pending U.S. Application Serial No. 08/044,812, incorporated by reference; a portion of this cDNA comprising the coding region was sequenced and is shown in Figures 5A and 5B (SEQ ID Nos:11 & 12).

**EXAMPLE 2F****Isolation of a Human MC-4 Receptor DNA**

For cloning the MC-4 receptor, a human genomic library was screened at moderate stringency (40% formamide, 1M NaCl, 50mM Tris-HCl, pH 7.5, 0.1% sodium pyrophosphate, 0.2% sodium dodecyl sulfate, 100 $\mu$ g/ml salmon sperm DNA, 10X Denhardt's solution, 42°C), using rat PCR fragments isolated as described in Example 1 herein, with the exception that the following primers were used for PCR: Primer II (sense):

GAGTCGACC(A/G)CCCATGTA(C/T)T(AGT)(C/T)TTCATCTG  
(SEQ ID NO:13)

and

Primer VII (antisense):

CAGAATTCGGAA(A/G)GC(A/G)TA(G/T)ATGA(A/G)GGGGTC  
(SEQ ID NO:14)

A genomic clone was isolated that encodes a highly related G-coupled receptor protein (SEQ ID NO:15 and Figures 6A and 6B) on a 1.9kb *Hind*III fragment. The predicted amino acid sequence (SEQ ID NO:16) of this clone is 55-61% sequence



identity with human MC-3 and MC-5 receptors, and 46-47% sequence identity with the human MC-1 and MC-2 (ACTH) receptor.

### EXAMPLE 2G

5

#### **Isolation of a Mouse MC-5 Receptor DNA**

One million clones from a mouse 129SVJ genomic library comprising 5,000,000 clones in the  $\lambda$ FixII vector (Stratagene) was screened at low stringency (hybridization in 40% formamide at 42°C, washing performed in 0.5X SSC at 60°C, as described above in Example 2E) using radiolabeled probed from the rat MC-3 and MC-4 receptors (as described in Examples 2E and 2F). Positively-hybridizing clones were isolated and sequenced, and the sequences obtained were compared to previously-isolated melanocortin receptor clones. One clone, comprising a previously-unknown sequence, was determined to encode the MC-5 melanocortin receptor. The nucleotide and amino acid sequences of this receptor are shown in Figures 7A and 7B (SEQ ID No.: 17 & 18).

15

### EXAMPLE 3

#### **Construction of a Recombinant Expression Construct, DNA Transfection and Functional Expression of the MCR Gene Products**

20

In order to produce recombinant mammalian cells expressing each of the melanocortin receptors of Example 2, cDNA from each receptor was cloned into a mammalian expression construct, the resulting recombinant expression construct transfected into human 293 cells, and cell lines generated that expressed the melanocortin receptor proteins in cellular membranes at the cell surface.

25

The mouse  $\alpha$ MSH receptor was cloned by excising the entire coding region of the  $\alpha$ MSH<sup>R</sup> (MC-1) cDNA insert comprising a 2.1kb fragment and subcloning this fragment into the *Bam*HI/*Xho*I sites of pcDNAI/neo expression vector (Invitrogen, San Diego, CA). The resulting plasmid was prepared in large-scale through one cycle of CsCl gradient ultracentrifugation, and 20  $\mu$ g of the plasmid transfected into each 100mm dish of 293 cells using the calcium phosphate method (*see* Chen & Okayama, 1987, *J. Biol. Chem.* 262: 2745-2752). After transfection, cells were cultured in DMEM media supplemented with 10% calf serum in a 3% CO<sub>2</sub> atmosphere at 37°C. Selection was

30

performed with neomycin (G418; GIBCO) at a concentration of 1000  $\mu\text{g/ml}$ ; selection was started 72 hr after transfection and continued for 3 weeks.

5 The  $\alpha\text{MSH}^R$  is known to couple to G-proteins and thereby activate adenyl cyclase, increasing intracellular levels of cAMP (*see* Buckley & Ramachandran, 1981, *Proc. Natl. Acad. Sci. USA* 78: 7431-7435; Grahame-Smith *et al.*, 1967, *J. Biol. Chem.* 242: 5535-5541; Mertz & Catt, 1991, *Proc. Natl. Acad. Sci. USA* 88: 8525-8529; Pawalek *et al.*, 1976, *Invest. Dermatol.* 66: 200-209). This property of cells expressing the  $\alpha\text{MSH}$  receptor was used to analyze expression of the  $\alpha\text{MSH}$  receptor in cell colonies transfected with the expression vectors described herein as follows. Cells  
10 ( $\sim 1 \times 10^6$ ) were plated in 6-well dishes, washed once with DMEM containing 1% bovine serum albumin (BSA) and 0.5mM IBMX (a phosphodiesterase inhibitor), then incubated for 45 minutes at 37°C with varying concentrations of the melanotropic peptides  $\alpha\text{MSH}$ ,  $\beta\text{MSH}$ ,  $\gamma\text{MSH}$ , the MSH peptide analogues Nle<sup>4</sup>, D-Phe<sup>7</sup>- $\alpha\text{MSH}$  (NDP-MSH), and ACTH. Following hormone treatment, the cells were washed twice  
15 with phosphate buffered saline and intracellular cAMP extracted by lysing the cells with 1ml of 60% ethanol. Intracellular cAMP concentrations were determined using an assay (Amersham) which measures the ability of cAMP to displace [8-<sup>3</sup>H] cAMP from a high affinity cAMP binding protein (*see* Gilman, 1970, *Proc. Natl. Acad. Sci. USA* 67: 305-312).

20 The results of these experiments are shown in Figure 8. The abscissa indicates the concentration of each hormone and the ordinate indicates the percentage of basal intracellular cAMP concentration achieved by each treatment. Points indicate the mean of duplicate incubations; the standard error did not exceed 15% for any data point. None of the peptides tested induced any change in intracellular cAMP in cells  
25 containing the vector alone. Cells expressing the murine  $\alpha\text{MSH}$  receptor responded to melanotropic peptides with a 2-3 fold elevation of intracellular cAMP, similar to levels of cAMP induced by these peptides in the Cloudman cell line (*see* Pawalek, 1985, *Yale J. Biol. Med.* 58: 571-578). The  $\text{EC}_{50}$  values determined for  $\alpha\text{MSH}$  ( $2.0 \times 10^{-9}\text{M}$ ), ACTH ( $8.0 \times 10^{-9}\text{M}$ ) and the superpotent MSH analogue NDP-MSH  
30 ( $2.8 \times 10^{-11}\text{M}$ ) correspond closely to reported values (*see* Tatro *et al.*, 1990, *Cancer Res.* 50: 1237-1242). As expected, the  $\beta\text{MSH}$  peptide had an  $\text{EC}_{50}$  value comparable

to  $\alpha$ MSH, while  $\gamma$ MSH had little or no activity (*see Slominski et al.*, 1992, *Life Sci.* 50: 1103-1108), confirming the identity of this receptor as a melanocyte  $\alpha$ MSH receptor.

A similar series of experiments were performed using mouse Y1 cells (subclone OS3; Schimmer *et al.*, 1995, *J. Cell. Physiol.* 163: 164-171) expressing the human and bovine MC-2 (ACTH) receptor clones of Examples 2C and 2D. These results are shown in Figure 9, where the extent of cAMP responsive element-linked  $\beta$ -galactosidase activity (*see Example 4, below*) is shown with increasing concentrations of ACTH.

The entire coding region of the MC-3 receptor cDNA insert, obtained as described above in the co-pending U.S. Serial No. 08/044,812, was contained in a 2.0kb restriction enzyme digestion fragment and was cloned into the *Bam*HI/*Xho*I sites of pcDNA/neo I expression vector (Invitrogen, San Diego, CA). The resulting plasmid was prepared in large-scale through one cycle of CsCl gradient ultracentrifugation and 20  $\mu$ g pcDNA/MC-3 receptor DNA were transfected into each 100 mm dish of 293 cells using the calcium phosphate method (*see Chen & Okayama*, 1987, *Mol. Cell. Biol.* 7: 2745-2752). After transfection, cells were cultured in DMEM media supplemented with 10% calf serum in a 3% CO<sub>2</sub> atmosphere at 37°C. Selection was performed with neomycin (G418; GIBCO) at a concentration of 1000  $\mu$ g/ml; selection was started 72 h after transfection and continued for 3 weeks.

Specific binding of melanocortin peptides to cells expressing the MC-3 receptor was demonstrated by competition experiments using <sup>125</sup>I-labeled Nle<sup>4</sup>-D-Phe<sup>7</sup>- $\alpha$ -MSH (NDP-MSH, as described in Tatro *et al.*, 1990, *Cancer Res.* 50: 1237-1242). Suspended cells (2x10<sup>5</sup>) were incubated at 37°C with 500,000 cpm of labeled peptide for 10 min in binding buffer (Ham's F10 media plus 10mM HEPES, pH 7.2, 0.25% bovine serum albumin, 500K IU/ml aprotinin, 100  $\mu$ g/ml bacitracin and 1mM 1,10-phenanthroline) in the presence or absence of the indicated concentrations of peptides. Maximum labeling was achieved within 10 min.

The results of these experiments are shown in Figure 10. Labeled NDP-MSH binding to cells expressing the MC-3 receptor, produced as described above, is inhibited by competition with unlabeled peptides known to be melanocortin receptor agonists, having a relative order of potency as follows:

NDP-MSH >  $\gamma$ -MSH >  $\alpha$ -MSH > ACTH<sub>4-10</sub> >>> ORG2766.

Approximate  $K_i$  values derived from this experiment are as shown in Table I:

TABLE I

Agonist	$K_i$ (approx)
NDP-MSH	$2 \times 10^{-8}$
$\gamma$ -MSH	$5 \times 10^{-8}$
$\alpha$ -MSH	$1 \times 10^{-7}$
ACTH <sub>4-10</sub>	$8 \times 10^{-5}$

cAMP production assays as described above were also used to analyze expression of MC3-R in cells transfected with the expression vectors described herein as follows. Cells ( $\sim 5 \times 10^6$ ) were plated in 6-well dishes, washed once with DMEM containing 1% bovine serum albumin (BSA) and 0.5mM IBMX (a phosphodiesterase inhibitor), then incubated for 1h at 37°C with varying concentrations of the melanotropic peptides  $\alpha$ MSH,  $\gamma_3$ MSH,  $\gamma$ MSH, the MSH peptide analogues Nle<sup>4</sup>-D-Phe<sup>7</sup>- $\alpha$ MSH (NDP-MSH), ACTH<sub>4-10</sub> and ACTH<sub>1-39</sub>. Following hormone treatment, the cells were washed twice with phosphate buffered saline and intracellular cAMP extracted by lysing the cells with 1ml of 60% ethanol. Intracellular cAMP concentrations were determined using an assay which measures the ability of cAMP to displace [8-<sup>3</sup>H] cAMP from a high affinity cAMP binding protein (see Gilman, 1979, *Proc. Natl. Acad. Sci. USA* 67: 305-312).

The results of these experiments are shown in Figures 11A through 11C. The abscissa indicates the concentration of each hormone and the ordinate indicates the percentage of basal intracellular cAMP concentration achieved by each treatment. Points indicate the mean of duplicate incubations; the standard error did not exceed 15% for any data point. Figure 11A depicts the results of experiments using peptides found *in vivo*; Figure 11B depicts results found with  $\gamma$ -MSH variants; and Figure 11C shows results of synthetic melanocortin analogues. None of the peptides tested induced any change in intracellular cAMP in cells containing the vector alone. Cells expressing rat MC3-R responded strongly to every melanotropic peptide containing the MSH sequence

His-Phe-Arg-Trp, with up to a 60-fold elevation of intracellular cAMP levels.  $EC_{50}$  values ranged from 1-50 nM. The most potent ligand and the one having the lowest  $EC_{50}$  was found to be  $\gamma$ MSH. The order of potency for the naturally occurring melanocortins was found to be:

- 5  $\gamma_2$ -MSH =  $\gamma$ MSH >  $\alpha$ MSH = ACTH<sub>1-39</sub> >  $\gamma_3$ -MSH > *des*-acetyl- $\alpha$ MSH > ACTH<sub>4-10</sub>.  
 $EC_{50}$  values for these compounds are shown in Table II:

TABLE II

Agonist	$EC_{50}$
NDP-MSH	$1 \times 10^{-9}$
$\gamma_1$ -MSH	$3 \times 10^{-9}$
$\gamma_2$ -MSH	$3 \times 10^{-9}$
$\alpha$ -MSH	$4 \times 10^{-9}$
15 ACTH <sub>1-39</sub>	$4 \times 10^{-9}$
$\gamma_3$ -MSH	$6 \times 10^{-9}$
<i>des</i> acetyl- $\alpha$ MSH	$8 \times 10^{-9}$
ACTH <sub>4-10</sub>	$1 \times 10^{-7}$

- 20 Additionally, a synthetic melanocortin peptide (ORG2766), known to have the greatest activity *in vivo* in stimulation of retention of learned behavior and in stimulation of neural regeneration, was unable to stimulate MC3-R-mediated cAMP production, and was also inactive as an antagonist. The results strongly indicate that this peptide does not bind to MC3-R protein.

- 25 The MC-4 receptor was cloned in a 1.9kb *Hind*III genomic DNA fragment after PCR amplification of a lambda phage clone into pcDNAI/Neo (Invitrogen). This plasmid was stably introduced into human 293 cells by calcium phosphate co-precipitation using standard techniques, and plasmid-containing cells selected in G418 containing media. Specificity of receptor-hormone binding was assayed using adenylate  
 30 cyclase activity as described above. The MC-4 receptor was found to couple to adenylate cyclase activity having the following pattern of agonist affinity:

NDP-MSH > *des*-acetyl- $\alpha$ -MSH >= ACTH<sub>1-39</sub> >=  $\alpha$ -MSH > >  $\gamma_2$ -MSH = ACTH<sub>4-10</sub>

whereas the synthetic ACTH<sub>4-9</sub> analogue ORG2766 showed no detectable binding to the MC-4 receptor. The results of adenylate cyclase activity assays are shown in Figure 12. EC<sub>50</sub> values for each of the tested MC-4 receptor agonists are as shown in Table III:

TABLE III

Agonist	EC <sub>50</sub>
NDP-MSH	$1.1 \times 10^{-11} \text{M}$
desacetyl- $\alpha$ MSH	$4.9 \times 10^{-10} \text{M}$
ACTH <sub>1-39</sub>	$6.8 \times 10^{-10} \text{M}$
$\alpha$ -MSH	$1.5 \times 10^{-9} \text{M}$
$\gamma_2$ -MSH	$> 10^{-7} \text{M}$
ACTH <sub>4-10</sub>	$> 10^{-7}$

A 1.6kb *ApaI-HindIII* fragment comprising the entire coding sequence of the mouse MC-5 melanocortin receptor disclosed in Example 2G above was cloned into the pcDNA/neo expression vector (Invitrogen) after PCR amplification of the lambda phage clone. This plasmid was stably introduced into human 293 cells by calcium phosphate co-precipitation using standard techniques, and plasmid-containing cells selected in G418 containing media. Specificity of receptor-hormone binding was assayed using adenylate cyclase activity as described above. The MC-5 receptor was found to couple to adenylate cyclase activity having the following pattern of agonist affinity:



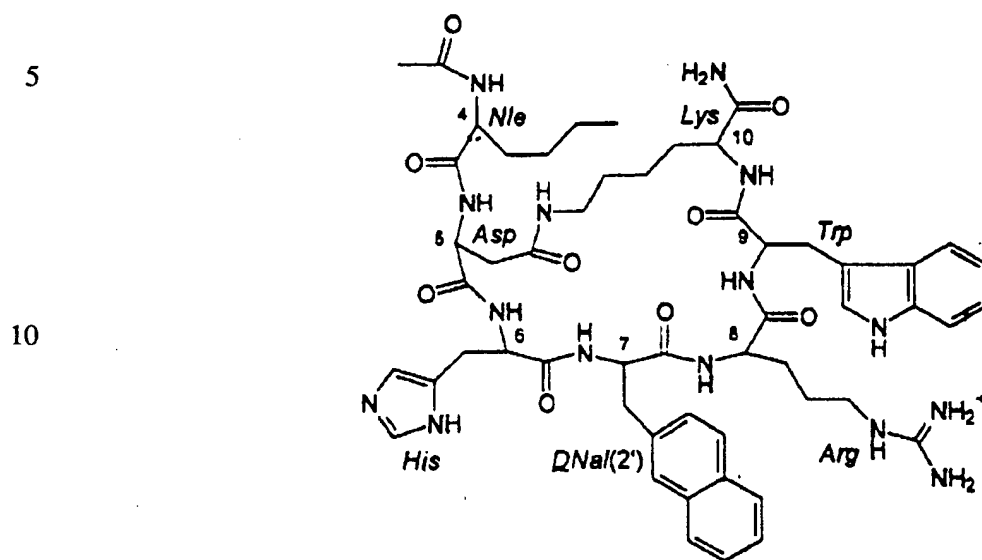
The results of adenylate cyclase activity assays are shown in Figure 13. EC<sub>50</sub> values for each of the tested MC-5 receptor agonists are:  $\alpha$ -MSH =  $1.7 \times 10^{-9} \text{M}$ ; and  $\beta$ MSH =  $5 \times 10^{-9} \text{M}$ .

#### EXAMPLE 4

##### Melanocortin Analogue Binding to Mammalian Melanocortin Receptors

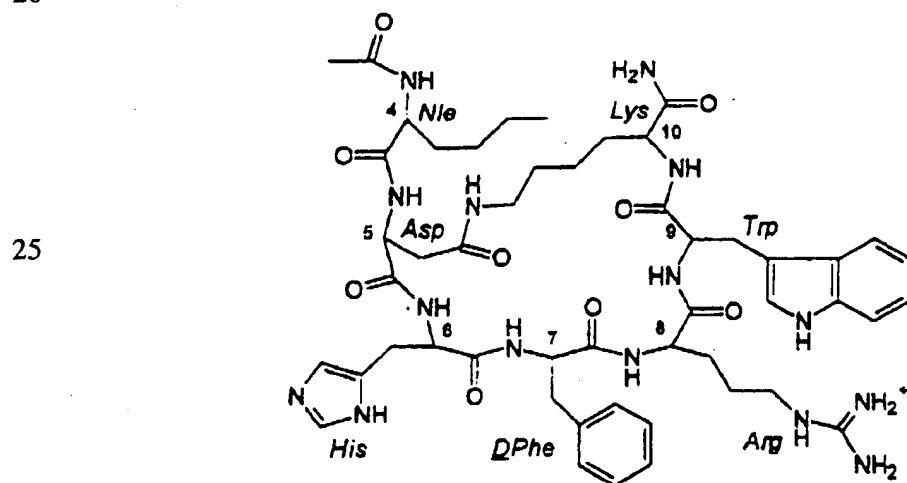
Recombinant cells prepared as described above in Example 3 were used to characterize receptor binding of two melanocortin analogues comprising cyclic lactam heptapeptides.

The melanocortin receptor analogue SHU9119 has the following chemical structure:



Ac-Nle<sup>4</sup>-cyclo(Asp<sup>5</sup>, D-Nal(2')<sup>7</sup>, Lys<sup>10</sup>) αMSH-(4-10)-amide

The melanocortin receptor analogue MTII has the following chemical structure:



Ac-Nle<sup>4</sup>-cyclo(Asp<sup>5</sup>, His<sup>6</sup>, D-Phe<sup>7</sup>, Arg<sup>8</sup>, Trp<sup>9</sup>, Lys<sup>10</sup>) αMSH-(4-10)-amide

These analogues were prepared as described in Hruby *et al.* (1995, *J. Med. Chem.* 38: 3454-3461).

These analogues were tested for melanocortin receptor binding using a colorimetric assay system developed by some of the instant inventors (Chen *et al.*, 1995, *Analyt. Biochem.* 226: 349-354) as follows. A series of concatamers of the synthetic oligonucleotide:

5'-GAATTCGACGTCACAGTATGACGGCCATGG-3'  
(SEQ ID No:19)

was produced by self-annealing and ligation and a tandem tetramer obtained. This fragment was cloned upstream of a fragment of the human vasoactive intestinal peptide (-93-+152; SEQ ID No.: 13; see Fink *et al.*, 1988, *Proc. Natl. Acad. Sci. USA* 85: 6662-6666). This promoter was then cloned upstream of the  $\beta$ -galactosidase gene from *E. coli*. The resulting plasmid construct is shown in Figure 14.

Transient transfection of the pCRE/ $\beta$ -gal plasmid described above was performed as follows. Cells grown to between 40-60% confluency (corresponding to about 1.5 million cells/6cm tissue culture plate) were incubated with Opti-MEM (GIBCO-BRL, Long Island, NY) and then contacted with a pCRE/ $\beta$ -gal-lipofectin complex which was prepared as follows. 3 $\mu$ g plasmid DNA and 20 $\mu$ L lipofectin reagent (GIBCO) were each diluted into 0.5mL Opti-MEM media and then mixed together. This mixture was incubated at room temperature for 15-20 min., and then the mixture (1mL) added to each 6cm plate. Transfected plates were incubated at 37°C for 5-24h, after which the plates were washed and incubated with DMEM media (GIBCO) and the cells split equally into a 96-well culture plate.

To assay melanocortin receptor analogue binding, human 293 cells expressing each of the melanocortin receptors MC-1, MC-3, MC-4 and MC-5, and mouse Y1 cells expressing the MC-2 receptor, were transiently transfected with pCRE/ $\beta$ -gal as described above and assayed as follows. Two days after transfection, cells were stimulated with hormones specific for each receptor or hormone analogue by incubation for 6h at 37°C with a mixture comprising  $10^{-12}$  -  $10^{-6}$ M hormone or analogue, 0.1mg/mL bovine serum albumin and 0.1mM isobutylmethylxanthine in DMEM. The effect of hormone or analogue binding was determined by  $\beta$ -galactosidase assay according to the method of Felgner *et al.* (1994, *J. Biol. Chem.* 269: 2550-2561). Briefly, media was aspirated from



culture wells and 50 $\mu$ L lysis buffer (0.25M Tris-HCl, pH 8/0.1% Triton-X100) added to each well. Cell lysis was enhanced by one round of freezing and thawing the cell/lysis buffer mixture. 10 $\mu$ L aliquots were sampled from each well for protein determination using a commercially-available assay (BioRad, Hercules, CA). The remaining 40 $\mu$ L from each well was diluted with 40 $\mu$ L phosphate buffered saline/0.5% BSA and 150 $\mu$ L substrate buffer (60mM sodium phosphate/ 1mM MgCl<sub>2</sub>/ 10mM KCl/ 5mM  $\beta$ -mercaptoethanol/ 2mg/mL *o*-nitrophenyl- $\beta$ -D-galactopyranoside) added. Plates were incubated at 37°C for 1h and then absorbance at 405nm determined using a 96-well plate reader (Molecular Devices, Sunnyvale, CA). A series of two-fold dilutions from 20ng of purified  $\beta$ -galactosidase protein (Sigma Chemical Co, St. Louis, MO) were assayed in parallel in each experiment to enable conversion of OD<sub>405</sub> to known quantity of  $\beta$ -galactosidase protein.

The results of these experiments are shown in Figure 15. This Figure shows the results of the  $\beta$ -galactosidase assay described above using cells expressing each of the MC-1, MC-3, MC-4 or MC-5 receptors and contacted with  $\alpha$ MSH or a variety of  $\alpha$ MSH analogues, including SHU9119. These results showed that SHU9119 had relatively weak agonist activity for both the human MC-3 and MC-4 receptors.

These results demonstrated the development of a colorimetric assay for cAMP accumulation as the result of melanocortin receptor binding to agonists and antagonists.

The action of MTII, SHU9119, and the endogenous mouse *agouti* peptide as agonists or antagonists of rodent MC receptors was first determined by examining their ability to elevate intracellular cAMP in 293 cell lines expressing the rat MC3-R or mouse MC4-R (expressed as IC<sub>50</sub> values representing ligand concentration required for half-maximal inhibition of binding of (I-125)-(Nle<sup>4</sup>, D-Phe<sup>7</sup>) $\alpha$ -MSH tracer). Agonist/antagonist activity was also shown by demonstrating inhibition of cAMP elevation by the potent  $\alpha$ -MSH analogue [Nle<sup>4</sup>, D-Phe<sup>7</sup>] $\alpha$ -MSH, using either a cAMP-responsive  $\beta$ -galactosidase reporter construct as described above, or by direct adenyl cyclase assay as described in Example 3 (wherein EC<sub>50</sub> values represent ligand concentration required for half-maximal activation of a cAMP-responsive  $\beta$ -galactosidase reporter). Competition binding experiments were determined as the amount of radioactivity bound in the presence of 5x10<sup>-6</sup>M unlabeled [Nle<sup>4</sup>, D-Phe<sup>7</sup>] $\alpha$ -MSH, and was typically 3-5% of total counts bound.

In these experiments, murine *agouti* peptide was produced using a baculovirus system as described by Lu *et al.* (1994, *Nature* 371: 799-802), with the modification that the *agouti* peptide was purified from baculovirus supernatants by 0.6M NaCl step elution from an EconoS cation exchange column (BioRad). *Agouti* peptide used in these assays was approximately 60% pure.

Competition binding assays were performed to determine whether SHU9119 had antagonist activity towards  $\alpha$ MSH binding to either the MC-3 or MC-4 receptors. These assays were performed as follows. Human 293 cells (100,000 cells/well in 24-well plates) expressing either the MC-3 or MC-4 receptors prepared as described above were incubated with a solution of 1mg/mL BSA in PBS containing 100,000cpm ( $3.1 \times 10^{-10}$ M [ $^{125}$ I](Nle<sup>4</sup>, D-Phe<sup>7</sup>) $\alpha$ MSH and varying concentrations of  $\alpha$ MSH, (Nle<sup>4</sup>, D-Phe<sup>7</sup>) $\alpha$ MSH or SHU9119. Cells were incubated for 30min at 37°C, washed twice with PBS-BSA, lysed with 0.5mL 0.5N NaOH, and counted using a  $\gamma$ -counter to quantitate the amount of bound [ $^{125}$ I](Nle<sup>4</sup>, D-Phe<sup>7</sup>) $\alpha$ MSH. Control experiments showed non-specific binding to occur at about 3-5% levels, and this was taken into account when analyzing the experimental results.

The SHU9119 analogue was found to be a potent antagonist of both the human MC-3 and MC-4 receptors, as shown in Figure 16. These assays showed pA<sub>2</sub> values of 8.3 and 9.3 for the human MC-3 and MC-4 receptors, respectively, as determined using the method of Schild (1947, *Brit. J. Pharmacol.* 2: 189-206). In contrast, no significant alteration in IC<sub>50</sub> values was detected in binding experiments using this analogue with either the MC-3 or MC-4 receptors (Figure 17).

The activity of the MTII analogue was also assayed for melanocortin receptor agonist activity. These results are shown in Figures 18A and 18B, and confirmed that the MTII analogue is a specific agonist of the MC-3 and MC-4 receptors.

Specific competition of [Nle<sup>4</sup>,D-Phe<sup>7</sup>] $\alpha$ -MSH binding to rat MC-3 receptor by *agouti* peptide was observed, although accurate IC<sub>50</sub> values could not be determined because the peptide preparation was not homogenous (results not shown). Specific competition of  $\alpha$ -MSH activation of human MC4-R by *agouti* was previously disclosed (Lu *et al.*, 1994, *Nature* 371: 799-802).

## EXAMPLE 5

**Feeding Behavior Effect of Melanocortin Analogue Binding in Brain**

The results shown in Example 4 above suggested a role in the regulation of feeding behavior in mammalian brain for MC receptor agonists and antagonists, in view of the antagonist properties of the *agouti* peptide at the MC-3 and MC-4 receptors. The *agouti* peptide was known to cause obesity when expressed ectopically in the mouse, and has been found to be a high affinity antagonist of the melanocyte stimulating hormone receptor (MC1-R) and of the hypothalamic MC-4 receptor (*see Lu et al., ibid.*). The former activity explained the inhibitory effect of the *agouti* peptide on eumelanin pigment synthesis. Similarly, it was hypothesized by the inventors that *agouti* causes obesity in mice by antagonizing hypothalamic MC-4 receptors. The cyclic melanocortin analogue, SHU9119, having been shown herein and elsewhere (Hruby *et al.*) to be a specific, high affinity antagonist of the central MC-3 and MC-4 receptors, was tested for the effect of direct administration to mouse brain on feeding behavior in the animals. Intracerebroventricular (ICV) administration of SHU9119 was performed to avoid any complications caused by inhibition of peptide traverse of the blood-brain barrier.

Briefly, male C57B1/6J mice (18-29g) were maintained on a normal 12hr/12hr light dark cycle with food (Purina mouse chow) and water *ad libitum*. Animals were housed individually for 24 hrs, distributed into experimental and control groups, avoiding any bias as a function of prior weight, then injected with vehicle or vehicle plus drug just prior to the onset of a 12hr light or dark cycle. Fasted animals were deprived of food from 18:00 to 10:30 hrs to stimulate feeding during the daytime experimental period. Animals were lightly anesthetized with halothane, and administered into one lateral ventricle 2  $\mu$ L of a solution of artificial cerebrospinal fluid alone (acsf, comprising 130mM NaCl, 27mM NaHCO<sub>3</sub>, 1.2mM Na<sub>2</sub>HPQ, 0.3mM NaH<sub>2</sub>PO<sub>4</sub>, 0.5mM Na<sub>2</sub>SO<sub>4</sub>, 1.0mM CaCl<sub>2</sub>, 1.0mM MgCl<sub>2</sub>, and 2.5mM KCl), or 6nmol SHU9119 in acsf. Freehand injections were performed as described by Laursen and Belknap (1986, *J. Pharmacol. Methods* 16: 355-357) with some modifications. A 10 $\mu$ l luertip syringe (Hamilton 701LT) was fitted with a 0.5 inch 27 gauge needle. Stiff tygon tubing was slipped over the needle to expose 3mm of the needle tip. The syringe was held at a 45° angle from the front of the skull with the bevel facing up. The coronal suture was found by lightly rubbing the needle over the skull. Maintaining the 45° angle, the needle

was then inserted 1-2mm lateral to the midline, using only mild pressure to insert and remove the needle. The compounds indicated in a 2µl volume of acsf were administered slowly over approximately 15 seconds, and the needle removed after 35 seconds. Animals were allowed to recover from anesthesia and placed into a cage containing a premeasured quantity of food pellets in a spill-free cup. Moribund animals were not included in the study.

Stimulation of feeding by intracerebroventricular administration of the melanocortin antagonist SHU9119 is shown in Figures 19A through 19C. Curves show cumulative food intake as a function of time following administration of the substances shown. Figure 19A shows stimulation of feeding by administration of SHU9119 just prior to lights off (19:00 hrs) to C57B1/6J mice fed *ad libitum*. Figure 19B, in contrast, shows no effect of morning (10:00 hrs) SHU9119 administration in C57B1/6J mice fed *ad libitum*. Figure 19C illustrates stimulation of daytime feeding by SHU9119 administration in fasted C57B1/6J mice. In deriving the data points comprising these Figures, food remaining was briefly removed and weighted at the time intervals indicated. Data points indicate the mean and bars indicate standard error. Significance of the effect over time was determined by ANOVA with repeated measures. Significance of drug effects at individual time points was determined by two-way ANOVA, and is indicated in each Figure (\*\*\*=P<0.001, \*\*=P<0.01, \*=P<0.05).

These results demonstrated that ICV administration of SHU9119 into one lateral ventricle of the C57B1/6J mouse just prior to lights out led to a mean 60% increase in food intake over 12 hrs (Figure 19A; P<0.005). In contrast, daytime food intake in animals fed *ad libitum* was not stimulated by administration of SHU9119 (Figure 19B). SHU9119-treatment did, however, significantly stimulate daytime food intake in animals fasted for 16 hrs prior to the experiment (Figure 19C; P<0.001). Stimulation of feeding was evident at approximately two hrs post-treatment, and continued for 12 hrs, to produce a mean 34% in food intake relative to vehicle-injected controls.

These results supported the hypothesis that *agouti* and/or SHU9119 stimulate feeding by antagonizing MC receptors in the central nervous system. To further test this hypothesis, a series of experiments were performed wherein MC receptor agonists were administered to animals primed by fasting to eat, to determine whether feeding in such animals could be inhibited by the MC receptor agonists. Animals were induced to feed

by food deprivation for 16h prior to ICV administration of the non-specific melanocortin agonist MTII. In these experiments, ICV injections in male C57B1/6J mice (20-30g) and the measurement of food intake were performed as described above.

5 Results of these experiments are shown in Figures 20A through 20C. In comparison to vehicle-injected animals, MTII was found to produce a potent inhibition of feeding within one hour after administration (Figure 20A) in a dose-responsive manner. Food intake was significantly inhibited for up to four hours following administration ( $P < 0.001$ ) at the highest dose administered (3nmol), and decreased food intake continued for the next four hours with normal rates of food intake resuming at  
10 about 8 hours after treatment. This dose-responsive inhibition of feeding had an  $IC_{50}$  at the two hour time point of approximately 0.5nmol (Figure 20B). However, inhibition of feeding with 3nmol MTII was completely blocked by co-administration of 6nmol SHU9119 (Figure 20C;  $P < 0.001$ ), demonstrating that the effect results specifically from agonist binding to the MC-4 and/or MC-3 receptor.

15 Locomotor assays were performed to determine whether the effects on feeding behavior observed in these mice were secondary to generalized behavioral effects caused by administration of these melanocortin analogues. The effects of MTII on locomotor activity were tested by placing vehicle or MTII-treated mice in sound and light-proof cages containing multiple light beam detectors. These assays were performed by first  
20 injecting 3nmol MTII or acsf as described above. At three hours (2:45-3:25) post-injection, 12 mice were placed into 12 separate boxes containing multiple infrared light sources and photodetectors. The boxes were contained within separate ventilated light and sound attenuating chambers (Coulbourn model E10-20). Disruption of the infrared beams, with a 10msec resolution, was tallied independently for each one minute time  
25 period in each cage. The results of these assays are shown in Figure 20D. Data points indicate the mean total activity (# of light breaks) for 6 animals in each experimental group. Four way ANOVA statistical analysis was used to analyze the data, and indicated an absence of a significant difference among the two groups.

30 Inhibition of feeding by MTII could not be explained by any apparent behavioral abnormalities, or any effect on arousal or locomotor activity. MTII-treated animals appeared alert and exhibited no unusual behavior relative to controls. At approximately three hours after ICV administration, MTII-treated animals exhibited locomotor activity

that was indistinguishable from vehicle-treated animals (Figure 20D). The higher initial activity, indicative of exploratory behavior, and continued locomotion over a 15 min period was indistinguishable between the two groups, indicating that the inhibition of feeding was not due to decreased locomotion or decreased arousal.

5           The administration of MTII also inhibited food intake in three other models of hyperphagia: the C57B1/6J-*Lep<sup>ob</sup>* mouse, a neuropeptide Y (NPY)-injected C57B1/6J mouse and a C57B1/6J-*A<sup>y</sup>* mouse. Figure 21A shows inhibition of feeding by intracerebroventricular administration of MTII in *A<sup>y</sup>* mice (females, 19-28gms). Figure 21B shows inhibition of feeding by intracerebroventricular administration of MTII in C57B1/6J mice (females, 21-25gm) stimulated to feed by co-administration of NPY. Figure 21C shows inhibition of feeding by intracerebroventricular administration of the MTII in *ob/ob* mice (females, 48-69 gms). Figure 21D shows inhibition of feeding in *ob/ob* mice by intraperitoneal administration of MTII (females, 40-45 gms). ICV injections and measurement of food intake were performed as described above, with the exception of NPY treated animals, which were not fasted prior to experimentation. Animals treated intraperitoneally received 100µl of a 1mM solution of MTII in saline, and vehicle injections consisted of the same amount of saline alone. Significance indicated for individual time points, determined as described above, was for 3nmol MTII vs. acsf (Figure 21A), 1.18 nmol NPY vs. 1.18 nmol NPY + 3 nmol MTII (Figure 21B), 3nmol MTII vs. acsf (Figure 21C), and 100 nmol MTII vs. saline (Figure 21D).

20           The hyperphagia in these models can be clearly seen by comparing the 12 hr food intake following a fast in vehicle-injected C57B1/6J (2.4g, Figure 19A), C57B1/6J-*A<sup>y</sup>* (3.7g, Figure 21A) and C57B1/6J-*Lep<sup>ob</sup>* (3.7g, Figure 21C) animals. As expected, MTII treatment inhibited food intake following a 16 hr fast in the C57B1/6J-*A<sup>y</sup>* mouse (Figure 21A; P<0.05). Interestingly, while food intake for the first four hours is significantly inhibited relative to vehicle-injected animals, it is also significantly less inhibited in the C57B1/6J-*A<sup>y</sup>* animal than in the C57B1/6J animal given the same 3nmol dose (*compare*, Figure 20A *versus* Figure 21A, 1-4 hrs; P<0.001). The decreased effectiveness of the agonist in the presence of the *A<sup>y</sup>* allele is consistent with the proposal that this allele results in chronic expression of *agouti* peptide melanocortin antagonist in the brain.

30           MTII, upon co-administration, also significantly inhibited the profound stimulation of feeding induced by NPY, measured over a three hr period (Figure 21C;

P<0.005). Co-administration of an approximately two-fold molar excess of MTII produced a 74% inhibition of NPY-stimulated food intake at the three hour time point.

Finally, MTII also inhibited hyperphagia due to absence of leptin in the C57B1/6J-*Lep<sup>ob</sup>* mouse (Figure 21C; P<0.001). MTII potently blocked feeding (Figure 20A) in these animals, in contrast to the less potent inhibition described above for the C57B1/6J-*A<sup>y</sup>* mouse.

The C57B1/6J-*Lep<sup>ob</sup>* animal was also used to test the ability of MTII to regulate feeding when administered peripherally. Moderate doses (100nmol) of MTII inhibited feeding in the C57B1/6J-*Lep<sup>ob</sup>* mouse (P<0.001) while low doses (10nmol) did not (date not shown). The kinetics were similar to those seen with ICV administration, with a potent inhibition of feeding for the first four hours. The 100-fold higher dose required peripherally, as well as the similar kinetics, suggest a primarily central nervous system-based mechanism of action of MTII.

These data show that melanocortinergic neurons exert a tonic inhibition of feeding behavior, and that disruption of this signal leads to hyperphagia. With regard to the recently-discovered leptin hormone made by adipocytes, which is generally expressed at elevated levels in obese humans and rodents (such as the C57B1/6J-*Lep<sup>ob</sup>* animal), the regulatory defect is understood to be an incapacity to respond properly to the leptin hormone signal. The instant results indicate that the melanocortins act independently, and physiologically "downstream," from the leptin hormone/receptor interaction, because it has been shown herein that melanocortin receptor agonists can potentially inhibit feeding in the C57B1/6J-*Lep<sup>ob</sup>* animal.

These results suggest that MC receptor agonists and antagonists can affect mammalian feeding behavior, and provide a means for determining candidate compounds for the development of effective pharmacological products directed towards alleviating such human ailments as obesity, anorexia and cachexia.

## EXAMPLE 6

### Use of MC Receptor-Expressing Recombinant Cells for Screening Compounds that Affect Feeding Behavior in Mammals

The results obtained in Example 5 indicated that cells expressing a variety of mammalian melanocortin receptors are useful for characterizing compounds as a first

step towards developing MC receptor agonists and antagonists for controlling feeding behavior in mammals, particularly obesity and overweight disorders in general, as well as anorexia, cachexia and other failure-to-thrive disorders.

5 A panel of mammalian melanocortin receptor-expressing recombinant cells are provided as described above in Example 3, wherein each member of the panel comprises appropriate mammalian cells, such as human 293 cells, comprising a recombinant expression construct encoding the MC-1, MC-2 (ACTH), MC-3, MC-4 or MC-5 receptor, the panel constructed to comprise cells functionally expressing each of these MC receptor proteins.

10 The panel is used as follows. Receptor agonist activity is assayed by transient or stable expression of a protein which produces a metabolite reporter molecule in response to receptor binding by any of the MC receptor proteins. An example of such a reporter system is the recombinant expression construct described in Example 4, wherein cAMP responsive elements (CREs) are operatively linked to a bacterially-  
15 derived  $\beta$ -galactosidase ( $\beta$ -gal) gene. In the event of receptor binding, cAMP is produced in the mammalian cell, and the CRE induces  $\beta$ -gal expression. When co-incubated with a colorless substrate for  $\beta$ -gal, receptor binding results in conversion of the colorless substrate to a blue-colored product, which can be easily scored visually or spectrophotometrically. Alternative reporter genes, such a luciferase, can also be used  
20 as reporter systems, provided that expression of the reporter molecule-producing protein is functionally linked to receptor binding of a test compound. Alternatively, cAMP production resulting from MC receptor binding can also be measured directly.

Assay panels are arranged so that agonist activity can be identified, quantitated and correlated with expression of each MC receptor. Automated assays using such  
25 panels are also envisioned, whereby the qualitative and quantitative detection of a reporter metabolite is detected in an array (such as a 96-well tissue culture plate) and the data collected and assembled into a computer data-base or other analytical program.

Antagonist activity is detected by a modification of the above assay. In this assay, the inhibition of cAMP production by a standardized amount of a known receptor  
30 agonist, specific for each receptor, is assayed in the presence of a putative antagonist compound. Production of metabolite reporter molecules and their qualitative and quantitative detection is achieved as described above, and the specificity and potency of



each antagonist compound characterized with regard to the degree of inhibition achieved for each receptor.

5 In view of the instant disclosure, MC-3/MC-4 receptor antagonists are expected to be useful to inhibit food intake in a hungry animal, and MC-3/MC-4 receptor agonists are expected to be useful to increase food intake in an animal. Alternative patterns of feeding behavior associated with different patterns of MC receptor agonist/antagonist activity can be determined using this assay.

10 Compounds having agonist or antagonist activity with the MC-3 or MC-4 receptors detected using this assay are further screened *in vivo* to determine whether the observed receptor binding activity results in modification of feeding behavior when administered to an animal. In these assays, the MC receptor binding compounds detected using the assay are administered intracranioventricularly as described above in Example 5 to animals after an overnight fast, to waking animals, or to animals that are not otherwise primed to be hungry. Feeding and locomotor activity is monitored in these animals, and compounds affecting eating behavior (either by inhibiting feeding in otherwise hungry animals or stimulating feeding in otherwise sated animals) are selected for further development.

15 In addition, systemic administration of compounds found to be active by ICV administration assays is used to screen such compounds for the ability to cross the blood-brain barrier. Such compounds are also useful as templates for modifications aimed at increasing the availability of these compounds in the brain after systemic administration, for increasing bioactivity, or both.

20 It should be understood that the foregoing disclosure emphasizes certain specific embodiments of the invention and that all modifications or alternatives equivalent thereto are within the spirit and scope of the invention as set forth in the appended claims.

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

## (i) APPLICANT:

- (A) NAME: Oregon Health Sciences University
- (B) STREET: 3181 S.W. Sam Jackson Park Road
- (C) CITY: Portland
- (D) STATE: Oregon
- (E) COUNTRY: USA
- (F) POSTAL CODE (ZIP): 97201
- (G) TELEPHONE: 503-494-8200
- (H) TELEFAX: 503-494-4729

- (ii) TITLE OF INVENTION: Methods and Reagents for Discovering and Using Mammalian Melanocortin Receptor Agonists and Antagonists To Modulate Feeding Behavior in Animals

- (iii) NUMBER OF SEQUENCES: 19

## (iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

## (v) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

## (ix) FEATURE:

- (A) NAME/KEY: mics\_feature
- (B) LOCATION: 1..35
- (D) OTHER INFORMATION: /function = "Degenerate oligonucleotide primer (sense)"  
/note= "The residue at positions 24 and 24 are inosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAGTCGACCT GTGYGYSATY RCNNTKGACM GSTAC

35

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: mics\_feature
- (B) LOCATION: 1..32
- (D) OTHER INFORMATION: /function = "Degenerate  
oligonucleotide primer (antisense)"  
/note= "The residue at position 18 is inosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CAGAATTCAG WAGGGCANCC AGCAGASRYG AA

32

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(ix) FEATURE:

- (A) NAME/KEY: 5'UTR
- (B) LOCATION: 1..14

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 15..959

(ix) FEATURE:

- (A) NAME/KEY: 3'UTR
- (B) LOCATION: 960..1260

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTCCTGACAA GACT ATG TCC ACT CAG GAG CCC CAG AAG AGT CTT CTG GGT	50
Met Ser Thr Gln Glu Pro Gln Lys Ser Leu Leu Gly	
1 5 10	
TCT CTC AAC TCC AAT GCC ACC TCT CAC CTT GGA CTG GCC ACC AAC CAG	98
Ser Leu Asn Ser Asn Ala Thr Ser His Leu Gly Leu Ala Thr Asn Gln	
15 20 25	
TCA GAG CCT TGG TGC CTG TAT GTG TCC ATC CCA GAT GGC CTC TTC CTC	146
Ser Glu Pro Trp Cys Leu Tyr Val Ser Ile Pro Asp Gly Leu Phe Leu	
30 35 40	
AGC CTA GGG CTG GTG AGT CTG GTG GAG AAT GTG CTG GTT GTG ATA GCC	194
Ser Leu Gly Leu Val Ser Leu Val Glu Asn Val Leu Val Val Ile Ala	
45 50 55 60	
ATC ACC AAA AAC CGC AAC CTG CAC TCG CCC ATG TAT TAC TTC ATC TGC	242
Ile Thr Lys Asn Arg Asn Leu His Ser Pro Met Tyr Tyr Phe Ile Cys	
65 70 75	
TGC CTG GCC CTG TCT GAC CTG ATG GTA AGT GTC AGC ATC GTG CTG GAG	290
Cys Leu Ala Leu Ser Asp Leu Met Val Ser Val Ser Ile Val Leu Glu	
80 85 90	
ACT ACT ATC ATC CTG CTG CTG GAG GTG GGC ATC CTG GTG GCC AGA GTG	338
Thr Thr Ile Ile Leu Leu Leu Glu Val Gly Ile Leu Val Ala Arg Val	
95 100 105	
GCT TTG GTG CAG CAG CTG GAC AAC CTC ATT GAC GTG CTC ATC TGT GGC	386
Ala Leu Val Gln Gln Leu Asp Asn Leu Ile Asp Val Leu Ile Cys Gly	
110 115 120	
TCC ATG GTG TCC AGT CTC TGC TTC CTG GGC ATC ATT GCT ATA GAC CGC	434
Ser Met Val Ser Ser Leu Cys Phe Leu Gly Ile Ile Ala Ile Asp Arg	
125 130 135 140	
TAC ATC TCC ATC TTC TAT GCG CTG CGT TAT CAC AGC ATC GTG ACG CTG	482
Tyr Ile Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu	
145 150 155	
CCC AGA GCA CGA CGG GCT GTC GTG GGC ATC TGG ATG GTC AGC ATC GTC	530
Pro Arg Ala Arg Arg Ala Val Val Gly Ile Trp Met Val Ser Ile Val	
160 165 170	
TCC AGC ACC CTC TTT ATC ACC TAC TAC AAG CAC ACA GCC GTT CTG CTC	578
Ser Ser Thr Leu Phe Ile Thr Tyr Tyr Lys His Thr Ala Val Leu Leu	
175 180 185	

TGC CTC GTC ACT TTC TTT CTA GCC ATG CTG GCA CTC ATG GCG ATT CTG Cys Leu Val Thr Phe Phe Leu Ala Met Leu Ala Leu Met Ala Ile Leu 190 195 200	626
TAT GCC CAC ATG TTC ACG AGA GCG TGC CAG CAC GTC CAG GGC ATT GCC Tyr Ala His Met Phe Thr Arg Ala Cys Gln His Val Gln Gly Ile Ala 205 210 215 220	674
CAG CTC CAC AAA AGG CGG CGG TCC ATC CGC CAA GGC TTC TGC CTC AAG Gln Leu His Lys Arg Arg Arg Ser Ile Arg Gln Gly Phe Cys Leu Lys 225 230 235	722
GGT GCT GCC ACC CTT ACT ATC CTT CTG GGG ATT TTC TTC CTG TGC TGG Gly Ala Ala Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp 240 245 250	770
GGC CCC TTC TTC CTG CAT CTC TTG CTC ATC GTC CTC TGC CCT CAG CAC Gly Pro Phe Phe Leu His Leu Leu Leu Ile Val Leu Cys Pro Gln His 255 260 265	818
CCC ACC TGC AGC TGC ATC TTC AAG AAC TTC AAC CTC TTC CTC CTC CTC Pro Thr Cys Ser Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Leu Leu 270 275 280	866
ATC GTC CTC AGC TCC ACT GTT GAC CCC CTC ATC TAT GCT TTC CGC AGC Ile Val Leu Ser Ser Thr Val Asp Pro Leu Ile Tyr Ala Phe Arg Ser 285 290 295 300	914
CAG GAG CTC CGC ATG ACA CTC AAG GAG GTG CTG CTG TGC TCC TGG Gln Glu Leu Arg Met Thr Leu Lys Glu Val Leu Leu Cys Ser Trp 305 310 315	959
TGATCAGAGG GCGCTGGGCA GAGGGTGACA GTGATATCCA GTGGCCTGCA TCTGTGAGAC	1019
CACAGGTACT CATCCCTTCC TGATCTCCAT TTGTCTAAGG GTCGACAGGA TGAGCTTTAA	1079
AATAGAAACC CAGAGTGCCT GGGGCCAGGA GAAAGGGTAA CTGTGACTGC AGGGCTCACC	1139
CAGGGCAGCT ACGGGAAGTG GAGGAGACAG GGATGGGAAC TCTAGCCCTG AGCAAGGGTC	1199
AGACCACAGG CTCCTGAAGA GCTTCACCTC TCCCCACCTA CAGGCAACTC CTGCTCAAGC	1259
C	1260

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Met Ser Thr Gln Glu Pro Gln Lys Ser Leu Leu Gly Ser Leu Asn Ser
 1              5              10              15

Asn Ala Thr Ser His Leu Gly Leu Ala Thr Asn Gln Ser Glu Pro Trp
      20              25              30

Cys Leu Tyr Val Ser Ile Pro Asp Gly Leu Phe Leu Ser Leu Gly Leu
      35              40              45

Val Ser Leu Val Glu Asn Val Leu Val Val Ile Ala Ile Thr Lys Asn
      50              55              60

Arg Asn Leu His Ser Pro Met Tyr Tyr Phe Ile Cys Cys Leu Ala Leu
      65              70              75              80

Ser Asp Leu Met Val Ser Val Ser Ile Val Leu Glu Thr Thr Ile Ile
      85              90              95

Leu Leu Leu Glu Val Gly Ile Leu Val Ala Arg Val Ala Leu Val Gln
      100              105              110

Gln Leu Asp Asn Leu Ile Asp Val Leu Ile Cys Gly Ser Met Val Ser
      115              120              125

Ser Leu Cys Phe Leu Gly Ile Ile Ala Ile Asp Arg Tyr Ile Ser Ile
      130              135              140

Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg Ala Arg
      145              150              155              160

Arg Ala Val Val Gly Ile Trp Met Val Ser Ile Val Ser Ser Thr Leu
      165              170              175

Phe Ile Thr Tyr Tyr Lys His Thr Ala Val Leu Leu Cys Leu Val Thr
      180              185              190

Phe Phe Leu Ala Met Leu Ala Leu Met Ala Ile Leu Tyr Ala His Met
      195              200              205

Phe Thr Arg Ala Cys Gln His Val Gln Gly Ile Ala Gln Leu His Lys
      210              215              220

Arg Arg Arg Ser Ile Arg Gln Gly Phe Cys Leu Lys Gly Ala Ala Thr
      225              230              235              240

Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro Phe Phe
      245              250              255

```

Leu His Leu Leu Leu Ile Val Leu Cys Pro Gln His Pro Thr Cys Ser  
                   260                                  265                                  270  
 Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Leu Leu Ile Val Leu Ser  
                   275                                  280                                  285  
 Ser Thr Val Asp Pro Leu Ile Tyr Ala Phe Arg Ser Gln Glu Leu Arg  
                   290                                  295                                  300  
 Met Thr Leu Lys Glu Val Leu Leu Cys Ser Trp  
 305                                  310                                  315

## (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1633 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

- (ix) FEATURE:
- (A) NAME/KEY: 5'UTR
  - (B) LOCATION: 1..461

- (ix) FEATURE:
- (A) NAME/KEY: CDS
  - (B) LOCATION: 462..1415

- (ix) FEATURE:
- (A) NAME/KEY: 3'UTR
  - (B) LOCATION: 1416..1633

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCCGCATGTG GCCGCCCTCA ATGGAGGGCT CTGAGAACGA CTTTAAAC GCAGAGAAAA	60
AGCTCCATTC TTCCAGACC TCAGCGCAGC CCTGGCCCAG GAAGGGAGGA GACAGAGGCC	120
AGGACGGTCC AGAGGTGTCG AAATGTCCTG GGAACCTGAG CAGCAGCCAC CAGGGAAGAG	180
GCAGGGAGGG AGCTGAGGAC CAGGCTTGGT TGTGAGAATC CCTGAGCCCA GGCGGTTGAT	240
GCCAGGAGGT GTCTGGACTG GCTGGGCCAT GCCTGGGCTG ACCTGTCCAG CCAGGGAGAG	300

GGTGTGAGGG CAGATCTGGG GGTGCCCAGA TGGAAGGAGG CAGGCATGGG GACACCCAAG	360
GGCCCCCTGGC AGCACCATGA ACTAAGCAGG ACACCTGGAG GGGAAGAACT GTGGGGACCT	420
GGAGGCCTCC AACGACTCCT TCCTGCTTCC TGGACAGGAC T ATG GCT GTG CAG	473
Met Ala Val Gln	
1	
GGA TCC CAG AGA AGA CTT CTG GGC TCC CTC AAC TCC ACC CCC ACA GCC	521
Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser Thr Pro Thr Ala	
5 10 15 20	
ATC CCC CAG CTG GGG CTG GCT GCC AAC CAG ACA GGA GCC CGG TGC CTG	569
Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly Ala Arg Cys Leu	
25 30 35	
GAG GTG TCC ATC TCT GAC GGG CTC TTC CTC AGC CTG GGG CTG GTG AGC	617
Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu Gly Leu Val Ser	
40 45 50	
TTG GTG GAG AAC GCG CTG GTG GTG GCC ACC ATC GCC AAG AAC CGG AAC	665
Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala Lys Asn Arg Asn	
55 60 65	
CTG CAC TCA CCC ATG TAC TGC TTC ATC TGC TGC CTG GCC TTG TCG GAC	713
Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu Ala Leu Ser Asp	
70 75 80	
CTG CTG GTG AGC GGG ACG AAC GTG CTG GAG ACG GCC GTC ATC CTC CTG	761
Leu Leu Val Ser Gly Thr Asn Val Leu Glu Thr Ala Val Ile Leu Leu	
85 90 95 100	
CTG GAG GCC GGT GCA CTG GTG GCC CGG GCT GCG GTG CTG CAG CAG CTG	809
Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val Leu Gln Gln Leu	
105 110 115	
GAC AAT GTC ATT GAC GTG ATC ACC TGC AGC TCC ATG CTG TCC AGC CTC	857
Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met Leu Ser Ser Leu	
120 125 130	
TGC TTC CTG GGC GCC ATC GCC GTG GAC CGC TAC ATC TCC ATC TTC TAC	905
Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile Ser Ile Phe Tyr	
135 140 145	
GCA CTG CGC TAC CAC AGC ATC GTG ACC CTG CCG CGG GCG CCG CGA GCC	953
Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg Ala Pro Arg Ala	
150 155 160	
GTT GCG GCC ATC TGG GTG GCC AGT GTC GTC TTC AGC ACG CTC TTC ATC	1001
Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser Thr Leu Phe Ile	
165 170 175 180	



GGC TAC TAC GAC CAC GTG GCC GTC CTG CTG TGC CTC GTG GTC TTC TTC	1049
Gly Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu Val Val Phe Phe	
185 190 195	
CTG GCT ATG CTG GTG CTC ATG GCC GTG CTG GAC GTC CAC ATG CTG GCC	1097
Leu Ala Met Leu Val Leu Met Ala Val Leu Asp Val His Met Leu Ala	
200 205 210	
CGG GCC TGC CAG CAC GCC CAG GGC ATC GCC CGG CTC CAC AAG AGG CAG	1145
Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu His Lys Arg Gln	
215 220 225	
CGC CCG GTC CAC CAG GGC TTT GGC CTT AAA GGC GCT GTC ACC CTC ACC	1193
Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala Val Thr Leu Thr	
230 235 240	
ATC CTG CTG GGC ATT TTC TTC CTC TGC TGG GGC CCC TTC TTC CTG CAT	1241
Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro Phe Phe Leu His	
245 250 255 260	
CTC ACA CTC ATC GTC CTC TGC CCC GAG CAC CCC ACG TGC GGC TGC ATC	1289
Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr Cys Gly Cys Ile	
265 270 275	
TTC AAG AAC TTC AAC CTC TTT CTC GCC CTC ATC ATC TGC AAT GCC ATC	1337
Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile Cys Asn Ala Ile	
280 285 290	
ATC GAC CCC CTC ATC TAC GCC TTC CAC AGC CAG GAG CTC CGC AGG ACG	1385
Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu Leu Arg Arg Thr	
295 300 305	
CTC AAG GAG GTG CTG ACA TGC TCC TGG TGA GCGCGGTGCA CGCGCTTTAA	1435
Leu Lys Glu Val Leu Thr Cys Ser Trp *	
310 315	
GTGTGCTGGG CAGAGGGAGG TGGTGATATT GTGGTCTGGT TCCTGTGTGA CCCTGGGCAG	1495
TTCCCTTACCT CCCTGGTCCC CGTTTGTCAG AGAGGATGGA CTAAATGATC TCTGAAAGTG	1555
TTGAAGCGCG GACCCTTCTG GGCAGGGAGG GGTCCTGCAA AACTCCAGGC AGGACTTCTC	1615
ACCAGCAGTC GTGGGAAC	1633

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
 1           5           10           15

Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
      20           25           30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
      35           40           45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
 50           55           60

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
 65           70           75           80

Ala Leu Ser Asp Leu Leu Val Ser Gly Thr Asn Val Leu Glu Thr Ala
      85           90           95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
     100           105           110

Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met
     115           120           125

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
     130           135           140

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg
     145           150           155           160

Ala Pro Arg Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
     165           170           175

Thr Leu Phe Ile Gly Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
     180           185           190

Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Asp Val
     195           200           205

His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
     210           215           220

His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
     225           230           235           240

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
     245           250           255

```

Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr  
                   260                                  265                                  270  
 Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile  
                   275                                  280                                  285  
 Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu  
                   290                                  295                                  300  
 Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Trp \*  
 305                                  310                                  315

## (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2012 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

- (ix) FEATURE:
- (A) NAME/KEY: 5'UTR
  - (B) LOCATION: 1..693

- (ix) FEATURE:
- (A) NAME/KEY: CDS
  - (B) LOCATION: 694..1587

- (ix) FEATURE:
- (A) NAME/KEY: 3'UTR
  - (B) LOCATION: 1588..2012

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ACAACACTTT ATATATATTT TTATAAATGT AAGGGGTACA AAGGTGCCAT TTTGTTACAT	60
GGATATACCG TG TAGTGGTG AAGCCTGGGC TTTTAGTGTA TCTGTCATCA GAATAACATA	120
CGTGTTACCC ATAGGAATTT CTCATCACCC GCCCCCTCCA CCCTTCGAGT CTCCAATGTC	180
CATTCCACAC TCTATATCCA CGTGTATGCA TATAGCTCCA CATATAAGTG AGAACATGTA	240
GTATTTGACT TCCTCTTTCT GAGTTATTTT ACTTTGATAA TGGCCTCCAC TTCCATCCAT	300
GTTGCTGCAA AAGACATGAC CTTATTCTTT TTGATAGCTG GGGAGTACTC CATTGTGTAT	360
ATGTACCACA TTTCTTTATC CATTACCCCA TTGAGAACAC TTAGTTGATT CCATATCTTT	420

GCTATTGTCA CTAGTGCTGC AATAAACATA CATGTGCAGG CTCCTTCTAA TATACTGATT	480
TATATTTTAT GGAGAGAGAT AGAGTTCTTA GCGAGTGTGC TGTTTATTTT TAGTGTACTT	540
GCAACTAATA TTCTGTATAC TCCCTTTAGG TGATTGGAGA TTAACTTAG ATCTCCAGCA	600
AGTGCTACAA GAAGAAAAGA TCCTGAAGAA TCAATCAAGT TTCCGTGAAG TCAAGTCCAA	660
GTAACATCCC CGCCTTAACC ACAAGCAGGA GAA ATG AAG CAC ATT ATC AAC TCG	714
Met Lys His Ile Ile Asn Ser	
1 5	
TAT GAA AAC ATC AAC AAC ACA GCA AGA AAT AAT TCC GAC TGT CCT CGT	762
Tyr Glu Asn Ile Asn Asn Thr Ala Arg Asn Asn Ser Asp Cys Pro Arg	
10 15 20	
TGT GTT TTG CCG GAG GAG ATA TTT TTC ACA ATT TCC ATT GTT GGA GTT	810
Cys Val Leu Pro Glu Glu Ile Phe Phe Thr Ile Ser Ile Val Gly Val	
25 30 35	
TTG GAG AAT CTG ATC GTC CTG CTG GCT GTG TTC AAG AAT AAG AAT CTC	858
Leu Glu Asn Leu Ile Val Leu Leu Ala Val Phe Lys Asn Lys Asn Leu	
40 45 50 55	
CAG GCA CCC ATG TAC TTT TTC ATC TGT AGC TTG GCC ATA TCT GAT ATG	906
Gln Ala Pro Met Tyr Phe Phe Ile Cys Ser Leu Ala Ile Ser Asp Met	
60 65 70	
CTG GGC AGC CTA TAT AAG ATC TTG GAA AAT ATC CTG ATC ATA TTG AGA	954
Leu Gly Ser Leu Tyr Lys Ile Leu Glu Asn Ile Leu Ile Ile Leu Arg	
75 80 85	
AAC ATG GGC ATA CTC AAG CCA CGT GGC AGT TTT GAA ACC ACA GCC CAT	1002
Asn Met Gly Ile Leu Lys Pro Arg Gly Ser Phe Glu Thr Thr Ala His	
90 95 100	
GAC ATC ATC GAC TCC CTG TTT CTG CTC TCC CGT CTT GGC TCC ATC TTC	1050
Asp Ile Ile Asp Ser Leu Phe Leu Leu Ser Arg Leu Gly Ser Ile Phe	
105 110 115	
GAC CTG CTC GTG ATT GCT GCG GAC CGC TAC ATC ACC ATC TTC CAC GCA	1098
Asp Leu Leu Val Ile Ala Ala Asp Arg Tyr Ile Thr Ile Phe His Ala	
120 125 130 135	
CTG CGG TAC CAC AGC ATC GTG ACC ATG CGC CGC ACT GTG GTG GTG CTT	1146
Leu Arg Tyr His Ser Ile Val Thr Met Arg Arg Thr Val Val Val Leu	
140 145 150	
ACG GTC ATC TGG ACG TTC TGC ACG GGG ACT GGC ATC ACC ATG GTG ATC	1194
Thr Val Ile Trp Thr Phe Cys Thr Gly Thr Gly Ile Thr Met Val Ile	
155 160 165	

TTC TCC CAT CAT GTG CCC CAC GTG ATC ACC TTC ACG TCG CTG TTC CCG	1242
Phe Ser His His Val Pro His Val Ile Thr Phe Thr Ser Leu Phe Pro	
170 175 180	
CTG ATG CTG GTC TTC ATC CTG TGC CTC TAT GTG CAC ATG TTC CTG CTG	1290
Leu Met Leu Val Phe Ile Leu Cys Leu Tyr Val His Met Phe Leu Leu	
185 190 195	
GCT CGA TGG CAC ACC AGG AAG ATC TCC ACC CTC CCC AGA GCC AAC ATG	1338
Ala Arg Trp His Thr Arg Lys Ile Ser Thr Leu Pro Arg Ala Asn Met	
200 205 210 215	
AAA GGG GCC ATG ACA CTG ACC ATC CTG CTC GGG GTC TTC ATC TTC TGC	1386
Lys Gly Ala Met Thr Leu Thr Ile Leu Leu Gly Val Phe Ile Phe Cys	
220 225 230	
TGG GCC CCC TTT GTG CTT CAT GTC CTC TTG ATG ACA TTC TGC CCA AGT	1434
Trp Ala Pro Phe Val Leu His Val Leu Leu Met Thr Phe Cys Pro Ser	
235 240 245	
AAC CCC TAC TGC GCC TGC TAC ATG TCT CTC TTC CAG GTG AAC GGC ATG	1482
Asn Pro Tyr Cys Ala Cys Tyr Met Ser Leu Phe Gln Val Asn Gly Met	
250 255 260	
TTG ATC ATG TGC AAT GCC GTC ATT GAC CCC TTC ATA TAT GCC TTC CGG	1530
Leu Ile Met Cys Asn Ala Val Ile Asp Pro Phe Ile Tyr Ala Phe Arg	
265 270 275	
AGC CCA GAG CTC AGG GAC GCA TTC AAA AAG ATG ATC TTC TGC AGC AGG	1578
Ser Pro Glu Leu Arg Asp Ala Phe Lys Lys Met Ile Phe Cys Ser Arg	
280 285 290 295	
TAC TGG TAG AATGGCTGAT CCCTGGTTTT AGAATCCATG GGAATAACGT	1627
Tyr Trp *	
TGCCAAGTGC CAGAATAGTG TAACATTCCA ACAAATGCCA GTGCTCCTCA CTGGCCTTCC	1687
TTCCCTAATG GATGCAAGGA TGACCCACCA GCTAGTGTTT CTGAATACTA TGGCCAGGAA	1747
CAGTCTATTG TAGGGGCAAC TCTATTTGTG ACTGGACAGA TAAAACGTGT AGTAAAAGAA	1807
GGATAGAATA CAAAGTATTA GGTACAAAAG TAATTAGGTT TGCATTACTT ATGACAAATG	1867
CATTACTTTT GCACCAATCT AGTAAAACAG CAATAAAAAT TCAAGGGCTT TGGGCTAAGG	1927
CAAAGACTTG CTTTCCTGTG GACATTAAAC AGCCAGTTCT GAGGCGGCCT TTCCAGGTGG	1987
AGGCCATTGC AGCCAATTTT AGAGT	2012

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```

Met Lys His Ile Ile Asn Ser Tyr Glu Asn Ile Asn Asn Thr Ala Arg
 1             5             10             15

Asn Asn Ser Asp Cys Pro Arg Cys Val Leu Pro Glu Glu Ile Phe Phe
      20             25             30

Thr Ile Ser Ile Val Gly Val Leu Glu Asn Leu Ile Val Leu Leu Ala
      35             40             45

Val Phe Lys Asn Lys Asn Leu Gln Ala Pro Met Tyr Phe Phe Ile Cys
      50             55             60

Ser Leu Ala Ile Ser Asp Met Leu Gly Ser Leu Tyr Lys Ile Leu Glu
      65             70             75             80

Asn Ile Leu Ile Ile Leu Arg Asn Met Gly Ile Leu Lys Pro Arg Gly
      85             90             95

Ser Phe Glu Thr Thr Ala His Asp Ile Ile Asp Ser Leu Phe Leu Leu
      100            105            110

Ser Arg Leu Gly Ser Ile Phe Asp Leu Leu Val Ile Ala Ala Asp Arg
      115            120            125

Tyr Ile Thr Ile Phe His Ala Leu Arg Tyr His Ser Ile Val Thr Met
      130            135            140

Arg Arg Thr Val Val Val Leu Thr Val Ile Trp Thr Phe Cys Thr Gly
      145            150            155            160

Thr Gly Ile Thr Met Val Ile Phe Ser His His Val Pro His Val Ile
      165            170            175

Thr Phe Thr Ser Leu Phe Pro Leu Met Leu Val Phe Ile Leu Cys Leu
      180            185            190

Tyr Val His Met Phe Leu Leu Ala Arg Trp His Thr Arg Lys Ile Ser
      195            200            205

Thr Leu Pro Arg Ala Asn Met Lys Gly Ala Met Thr Leu Thr Ile Leu
      210            215            220

```

Leu	Gly	Val	Phe	Ile	Phe	Cys	Trp	Ala	Pro	Phe	Val	Leu	His	Val	Leu
225					230					235					240
Leu	Met	Thr	Phe	Cys	Pro	Ser	Asn	Pro	Tyr	Cys	Ala	Cys	Tyr	Met	Ser
				245					250					255	
Leu	Phe	Gln	Val	Asn	Gly	Met	Leu	Ile	Met	Cys	Asn	Ala	Val	Ile	Asp
			260					265					270		
Pro	Phe	Ile	Tyr	Ala	Phe	Arg	Ser	Pro	Glu	Leu	Arg	Asp	Ala	Phe	Lys
		275					280					285			
Lys	Met	Ile	Phe	Cys	Ser	Arg	Tyr	Trp	*						
290						295									

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1108 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA to mRNA

(ix) FEATURE:

- (A) NAME/KEY: 5'UTR  
(B) LOCATION: 1..132

(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 133..1026

(ix) FEATURE:

- (A) NAME/KEY: 3'UTR  
(B) LOCATION: 1027..1106

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGGCCAGAA	AGTTCCTGCT	TCAGAGCAGA	AGATCTTCAG	CAAGAACTAC	AAAGAAGAAA	60								
AGATTCTGGA	GAATCAATCA	AGTTTCCTGT	CAAGTTCCAG	TAACGTTTCT	GTCTTAACTG	120								
CACACAGGAA	AG	ATG	AAA	CAC	ATT	CTC	AAT	CTG	TAT	GAA	AAC	CTC	AAC	168
	Met	Lys	His	Ile	Leu	Asn	Leu	Tyr	Glu	Asn	Leu	Asn		
	1				5				10					

AGT	ACA	GCA	AGA	AAT	AAC	TCA	GAC	TGT	CCT	GCT	GTG	ATT	TTG	CCA	GAA	216
Ser	Thr	Ala	Arg	Asn	Asn	Ser	Asp	Cys	Pro	Ala	Val	Ile	Leu	Pro	Glu	
		15					20					25				
GAG	ATA	TTT	TTC	ACA	GTA	TCC	ATT	GTT	GGG	GTT	TTG	GAG	AAC	CTG	ATG	264
Glu	Ile	Phe	Phe	Thr	Val	Ser	Ile	Val	Gly	Val	Leu	Glu	Asn	Leu	Met	
	30					35				40						
GTC	CTT	CTG	GCT	GTG	GCC	AAG	AAT	AAG	ATG	CTT	CAG	TCG	CCC	ATG	TAC	312
Val	Leu	Leu	Ala	Val	Ala	Lys	Asn	Lys	Met	Leu	Gln	Ser	Pro	Met	Tyr	
	45				50				55						60	
TTT	TTC	ATC	TGC	AGC	TTG	GCT	ATT	TCC	GAT	ATG	CTG	GGG	AGC	ATG	TAC	360
Phe	Phe	Ile	Cys	Ser	Leu	Ala	Ile	Ser	Asp	Met	Leu	Gly	Ser	Met	Tyr	
			65					70					75			
AAG	ATT	TTG	GAA	AAC	GTT	CTG	ATC	ATG	TTC	AAA	AAC	ATG	GGT	TAC	CTC	408
Lys	Ile	Leu	Glu	Asn	Val	Leu	Ile	Met	Phe	Lys	Asn	Met	Gly	Tyr	Leu	
		80						85				90				
GAG	CCT	CGA	GGC	AGT	TTT	GAA	AGC	ACA	GCA	GAT	GAT	GTG	GTG	GAC	TCC	456
Glu	Pro	Arg	Gly	Ser	Phe	Glu	Ser	Thr	Ala	Asp	Asp	Val	Val	Asp	Ser	
		95				100						105				
CTG	TTC	ATC	CTC	TCC	CTT	CTC	GGC	TCC	ATC	TGC	AGC	CTG	TCT	GTG	ATT	504
Leu	Phe	Ile	Leu	Ser	Leu	Leu	Gly	Ser	Ile	Cys	Ser	Leu	Ser	Val	Ile	
	110					115				120						
GCC	GCT	GAC	CGC	TAC	ACT	ACA	ATC	TTC	CAC	GCT	CTG	CAG	TAC	CAC	CGC	552
Ala	Ala	Asp	Arg	Tyr	Thr	Thr	Ile	Phe	His	Ala	Leu	Gln	Tyr	His	Arg	
	125				130				135						140	
ATC	ATG	ACC	CCC	GCA	CCG	TGC	CCT	CGT	CAT	CTG	ACG	GTC	CTC	TGG	CGA	600
Ile	Met	Thr	Pro	Ala	Pro	Cys	Pro	Arg	His	Leu	Thr	Val	Leu	Trp	Arg	
			145					150					155			
GGC	TGC	ACA	GGC	AGT	GGC	ATT	ACC	ATC	GTG	ACC	TTC	TCC	CAT	CAC	GTC	648
Gly	Cys	Thr	Gly	Ser	Gly	Ile	Thr	Ile	Val	Thr	Phe	Ser	His	His	Val	
		160						165					170			
CCC	ACA	GTG	ATC	GCC	TTC	ACA	GCG	CTG	TTC	CCG	CTG	ATG	CTG	GCC	TTC	696
Pro	Thr	Val	Ile	Ala	Phe	Thr	Ala	Leu	Phe	Pro	Leu	Met	Leu	Ala	Phe	
		175					180					185				
ATC	CTG	TGC	CTC	TAC	GTG	CAC	ATG	TTC	CTG	CTG	GCC	CGC	TCC	CAC	ACC	744
Ile	Leu	Cys	Leu	Tyr	Val	His	Met	Phe	Leu	Leu	Ala	Arg	Ser	His	Thr	
	190					195					200					
AGG	AGG	ACC	CCC	TCC	CTT	CCC	AAA	GCC	AAC	ATG	AGA	GGG	GCC	GTC	ACA	792
Arg	Arg	Thr	Pro	Ser	Leu	Pro	Lys	Ala	Asn	Met	Arg	Gly	Ala	Val	Thr	
	205				210					215				220		



CTG ACT GTC CTG CTC GGG GTC TTC ATT TTC TGT TGG GCA CCC TTT GTC	840
Leu Thr Val Leu Leu Gly Val Phe Ile Phe Cys Trp Ala Pro Phe Val	
225 230 235	
CTT CAT GTC CTC TTG ATG ACA TTC TGC CCA GCT GAC CCC TAC TGT GCC	888
Leu His Val Leu Leu Met Thr Phe Cys Pro Ala Asp Pro Tyr Cys Ala	
240 245 250	
TGC TAC ATG TCC CTC TTC CAG GTG AAT GGT GTG TTG ATC ATG TGT AAT	936
Cys Tyr Met Ser Leu Phe Gln Val Asn Gly Val Leu Ile Met Cys Asn	
255 260 265	
GCC ATC ATC GAC CCC TTC ATA TAT GCC TTT CGG AGC CCA GAG CTC AGG	984
Ala Ile Ile Asp Pro Phe Ile Tyr Ala Phe Arg Ser Pro Glu Leu Arg	
270 275 280	
GTC GCA TTC AAA AAG ATG GTT ATC TGC AAC TGT TAC CAG TAG	1026
Val Ala Phe Lys Lys Met Val Ile Cys Asn Cys Tyr Gln *	
285 290 295	
AATGATTGGT CCCTGATTTT AGGAGCCACA GGGATATACT GTCAGGGACA GAGTAGCGTG	1086
ACAGACCAAC AACACTAGGA CT	1108

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Lys His Ile Leu Asn Leu Tyr Glu Asn Leu Asn Ser Thr Ala Arg	
1 5 10 15	
Asn Asn Ser Asp Cys Pro Ala Val Ile Leu Pro Glu Glu Ile Phe Phe	
20 25 30	
Thr Val Ser Ile Val Gly Val Leu Glu Asn Leu Met Val Leu Leu Ala	
35 40 45	
Val Ala Lys Asn Lys Met Leu Gln Ser Pro Met Tyr Phe Phe Ile Cys	
50 55 60	
Ser Leu Ala Ile Ser Asp Met Leu Gly Ser Met Tyr Lys Ile Leu Glu	
65 70 75 80	

```

Asn Val Leu Ile Met Phe Lys Asn Met Gly Tyr Leu Glu Pro Arg Gly
      85                      90                      95

Ser Phe Glu Ser Thr Ala Asp Asp Val Val Asp Ser Leu Phe Ile Leu
      100                      105                      110

Ser Leu Leu Gly Ser Ile Cys Ser Leu Ser Val Ile Ala Ala Asp Arg
      115                      120                      125

Tyr Thr Thr Ile Phe His Ala Leu Gln Tyr His Arg Ile Met Thr Pro
      130                      135                      140

Ala Pro Cys Pro Arg His Leu Thr Val Leu Trp Arg Gly Cys Thr Gly
      145                      150                      155                      160

Ser Gly Ile Thr Ile Val Thr Phe Ser His His Val Pro Thr Val Ile
      165                      170                      175

Ala Phe Thr Ala Leu Phe Pro Leu Met Leu Ala Phe Ile Leu Cys Leu
      180                      185                      190

Tyr Val His Met Phe Leu Leu Ala Arg Ser His Thr Arg Arg Thr Pro
      195                      200                      205

Ser Leu Pro Lys Ala Asn Met Arg Gly Ala Val Thr Leu Thr Val Leu
      210                      215                      220

Leu Gly Val Phe Ile Phe Cys Trp Ala Pro Phe Val Leu His Val Leu
      225                      230                      235                      240

Leu Met Thr Phe Cys Pro Ala Asp Pro Tyr Cys Ala Cys Tyr Met Ser
      245                      250                      255

Leu Phe Gln Val Asn Gly Val Leu Ile Met Cys Asn Ala Ile Ile Asp
      260                      265                      270

Pro Phe Ile Tyr Ala Phe Arg Ser Pro Glu Leu Arg Val Ala Phe Lys
      275                      280                      285

Lys Met Val Ile Cys Asn Cys Tyr Gln *
      290                      295

```

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(ix) FEATURE:

(A) NAME/KEY: 5'UTR

(B) LOCATION: 1..297

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 298..1269

(ix) FEATURE:

(A) NAME/KEY: 3'UTR

(B) LOCATION: 1270..1338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGCTGTAACT GTAGCAACCG GTGTTGGGTG GGGATGAGAA GAGACCAGAG AGAGAGAGGG	60
TCAGAGCGAC AGGGGATGAG ACAGGCTGGT CAGAGTCTGC ACTGATTGTT GGAGACGCAA	120
AGGAAAGTTT TTTCTATGTC TCCAACCTCC CCTCCTCCC CCGTTTCTCT CTGGAGAAAC	180
TAAATGTAG ACTGGACAGC ATCCACAAGA GAAGCACCTA GAAGAAGATT TTTTTTCCC	240
AGCAGCTTGC TCAGGACCCT GCAGGAGCTG CAGCCGGAAC TGGTCCCGCC GATAACC	297
ATG AAC TCT TCC TGC TGC CCG TCC TCC TCT TAT CCG ACG CTG CCT AAC	345
Met Asn Ser Ser Cys Cys Pro Ser Ser Ser Tyr Pro Thr Leu Pro Asn	
1 5 10 15	
CTC TCC CAG CAC CCT GCA GCC CCC TCT GCC AGC AAC CGG AGT GGC AGT	393
Leu Ser Gln His Pro Ala Ala Pro Ser Ala Ser Asn Arg Ser Gly Ser	
20 25 30	
GGG TTC TGC GAG CAG GTT TTC ATC AAG CCA GAG GTC TTC CTG GCA CTG	441
Gly Phe Cys Glu Gln Val Phe Ile Lys Pro Glu Val Phe Leu Ala Leu	
35 40 45	
GGC ATC GTC AGT CTG ATG GAA AAC ATC CTG GTG ATC CTG GCT GTG GTG	489
Gly Ile Val Ser Leu Met Glu Asn Ile Leu Val Ile Leu Ala Val Val	
50 55 60	
AGG AAC GGC AAC CTG CAC TCC CCC ATG TAC TTC TTC CTG CTG AGC CTG	537
Arg Asn Gly Asn Leu His Ser Pro Met Tyr Phe Phe Leu Leu Ser Leu	
65 70 75 80	
CTG CAG GCC GAC CTG CTG GTG AGC CTG TCC AAC TCC CTG GAG ACC ATC	585
Leu Gln Ala Asp Leu Leu Val Ser Leu Ser Asn Ser Leu Glu Thr Ile	
85 90 95	

ATG ATC GTG GTT ATC AAC AGC GAC TCC CTG ACC TTG GAG GAC CAA TTC	633
Met Ile Val Val Ile Asn Ser Asp Ser Leu Thr Leu Glu Asp Gln Phe	
100 105 110	
ATC CAG CAC ATG GAC AAC ATC TTC GAC TCT ATG ATC TGC ATC TCC CTG	681
Ile Gln His Met Asp Asn Ile Phe Asp Ser Met Ile Cys Ile Ser Leu	
115 120 125	
GTG GCC TCC ATC TGC AAC CTC CTG GCC ATC GCC GTG GAC AGG TAC GTC	729
Val Ala Ser Ile Cys Asn Leu Leu Ala Ile Ala Val Asp Arg Tyr Val	
130 135 140	
ACC ATC TTC TAT GCC CTC CGT TAC CAC AGC ATC ATG ACG GTT AGG AAA	777
Thr Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Met Thr Val Arg Lys	
145 150 155 160	
GCC CTC TCC TTG ATC GTG GCC ATC TGG GTC TGC TGT GGC ATC TGC GGC	825
Ala Leu Ser Leu Ile Val Ala Ile Trp Val Cys Cys Gly Ile Cys Gly	
165 170 175	
GTG ATG TTC ATC GTC TAC TCC GAG AGC AAG ATG GTC ATC GTG TGC CTC	873
Val Met Phe Ile Val Tyr Ser Glu Ser Lys Met Val Ile Val Cys Leu	
180 185 190	
ATC ACC ATG TTC TTC GCC ATG GTG CTC CTC ATG GGC ACC CTG TAC ATC	921
Ile Thr Met Phe Phe Ala Met Val Leu Leu Met Gly Thr Leu Tyr Ile	
195 200 205	
CAC ATG TTC CTC TTC GCC AGG CTG CAC GTC CAG CGC ATC GCG GCA CTG	969
His Met Phe Leu Phe Ala Arg Leu His Val Gln Arg Ile Ala Ala Leu	
210 215 220	
CCA CCT GCT GAC GGG CTA GCC CCG CAG CAG CAC TCG TGC ATG AAG GGG	1017
Pro Pro Ala Asp Gly Leu Ala Pro Gln Gln His Ser Cys Met Lys Gly	
225 230 235 240	
GCC GTC ACC ATC ACC ATC CTG CTG GGG GTT TTC ATC TTC TGC TGG GCG	1065
Ala Val Thr Ile Thr Ile Leu Leu Gly Val Phe Ile Phe Cys Trp Ala	
245 250 255	
CCT TTC TTC CTC CAC CTG GTC CTC ATC ATC ACC TGC CCC ACC AAC CCC	1113
Pro Phe Phe Leu His Leu Val Leu Ile Ile Thr Cys Pro Thr Asn Pro	
260 265 270	
TAC TGC ATC TGC TAC ACG GCG CAC TTC AAC ACC TAC CTG GTT CTC ATC	1161
Tyr Cys Ile Cys Tyr Thr Ala His Phe Asn Thr Tyr Leu Val Leu Ile	
275 280 285	
ATG TGC AAC TCT GTC ATC GAC CCC CTC ATC TAC GCC TTC CGC AGC CTG	1209
Met Cys Asn Ser Val Ile Asp Pro Leu Ile Tyr Ala Phe Arg Ser Leu	
290 295 300	

GAG CTG CGA AAC ACC TTC AAG GAG ATT CTC TGC GGT TGC AAT GGC ATG 1257  
 Glu Leu Arg Asn Thr Phe Lys Glu Ile Leu Cys Gly Cys Asn Gly Met  
 305 310 315 320

AAC GTG GGC TAG GAACCCCGA GGAGGTGTTT CACGGCTAGC CAAGAGAGAA 1309  
 Asn Val Gly \*

AAGCAATGCT CAGGTGAGAC ACAGAAGGG 1338

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Asn	Ser	Ser	Cys	Cys	Pro	Ser	Ser	Ser	Tyr	Pro	Thr	Leu	Pro	Asn	1	5	10	15
Leu	Ser	Gln	His	Pro	Ala	Ala	Pro	Ser	Ala	Ser	Asn	Arg	Ser	Gly	Ser	20	25	30	
Gly	Phe	Cys	Glu	Gln	Val	Phe	Ile	Lys	Pro	Glu	Val	Phe	Leu	Ala	Leu	35	40	45	
Gly	Ile	Val	Ser	Leu	Met	Glu	Asn	Ile	Leu	Val	Ile	Leu	Ala	Val	Val	50	55	60	
Arg	Asn	Gly	Asn	Leu	His	Ser	Pro	Met	Tyr	Phe	Phe	Leu	Leu	Ser	Leu	65	70	75	80
Leu	Gln	Ala	Asp	Leu	Leu	Val	Ser	Leu	Ser	Asn	Ser	Leu	Glu	Thr	Ile	85	90	95	
Met	Ile	Val	Val	Ile	Asn	Ser	Asp	Ser	Leu	Thr	Leu	Glu	Asp	Gln	Phe	100	105	110	
Ile	Gln	His	Met	Asp	Asn	Ile	Phe	Asp	Ser	Met	Ile	Cys	Ile	Ser	Leu	115	120	125	
Val	Ala	Ser	Ile	Cys	Asn	Leu	Leu	Ala	Ile	Ala	Val	Asp	Arg	Tyr	Val	130	135	140	
Thr	Ile	Phe	Tyr	Ala	Leu	Arg	Tyr	His	Ser	Ile	Met	Thr	Val	Arg	Lys	145	150	155	160

Ala Leu Ser Leu Ile Val Ala Ile Trp Val Cys Cys Gly Ile Cys Gly  
                     165                    170                    175  
 Val Met Phe Ile Val Tyr Ser Glu Ser Lys Met Val Ile Val Cys Leu  
                     180                    185                    190  
 Ile Thr Met Phe Phe Ala Met Val Leu Leu Met Gly Thr Leu Tyr Ile  
                     195                    200                    205  
 His Met Phe Leu Phe Ala Arg Leu His Val Gln Arg Ile Ala Ala Leu  
                     210                    215                    220  
 Pro Pro Ala Asp Gly Leu Ala Pro Gln Gln His Ser Cys Met Lys Gly  
                     225                    230                    235                    240  
 Ala Val Thr Ile Thr Ile Leu Leu Gly Val Phe Ile Phe Cys Trp Ala  
                     245                    250                    255  
 Pro Phe Phe Leu His Leu Val Leu Ile Ile Thr Cys Pro Thr Asn Pro  
                     260                    265                    270  
 Tyr Cys Ile Cys Tyr Thr Ala His Phe Asn Thr Tyr Leu Val Leu Ile  
                     275                    280                    285  
 Met Cys Asn Ser Val Ile Asp Pro Leu Ile Tyr Ala Phe Arg Ser Leu  
                     290                    295                    300  
 Glu Leu Arg Asn Thr Phe Lys Glu Ile Leu Cys Gly Cys Asn Gly Met  
                     305                    310                    315                    320  
 Asn Val Gly \*

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (ix) FEATURE:

- (A) NAME/KEY: mics\_feature
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /function = "Degenerate  
oligonucleotide primer (sense)"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGTCGACCR CCCATGTAYT DYTTCATCTG

30

## (2) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1671 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA to mRNA

## (ix) FEATURE:

- (A) NAME/KEY: 5'UTR
- (B) LOCATION: 1..393

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 394..1389

## (ix) FEATURE:

- (A) NAME/KEY: 3'UTR
- (B) LOCATION: 1390..1671

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AGCTTCCGAG AGGCAGCCGA TGTGAGCATG TGCACACAGA TTCGTCTCCC AATGGCATGG	60
CAGCTTCAAG GAAAATTATT TTGAACAGAC TTGAATGCAT AAGATTAAAG TTAAAGCAGA	120
AGTGAGAACA AGAAAGCAAA GAGCAGACTC TTTCAACTGA GAATGAATAT TTTGAAGCCC	180
AAGATTTTAA CGTGATGATG ATTAGAGTCG TACCTAAAAG AGACTAAAAA CTCCATGTCA	240
AGCTCTGGAC TTGTGACATT TACTCACAGC AGGCATGGCA ATTTTAGCCT CACAACTTTC	300
AGACAGATAA AGACTTGGAG GAAATAACTG AGACGACTCC CTGACCCAGG AGGTTAAATC	360
AATTCAGGGG GACACTGGAA TTCTCCTGCC AGC ATG GTG AAC TCC ACC CAC CGT	414
Met Val Asn Ser Thr His Arg	
1 5	
GGG ATG CAC ACT TCT CTG CAC CTC TGG AAC CGC AGC AGT TAC AGA CTG	462
Gly Met His Thr Ser Leu His Leu Trp Asn Arg Ser Ser Tyr Arg Leu	
10 15 20	
CAC AGC AAT GCC AGT GAG TCC CTT GGA AAA GGC TAC TCT GAT GGA GGG	510
His Ser Asn Ala Ser Glu Ser Leu Gly Lys Gly Tyr Ser Asp Gly Gly	
25 30 35	

TGC TAC GCG CAA CTT TTT GTC TCT CCT GAG GTG TTT GTG ACT CTG GGT	558
Cys Tyr Ala Gln Leu Phe Val Ser Pro Glu Val Phe Val Thr Leu Gly	
40 45 50 55	
GTG ATC AGC TTG TTG GAG AAT ATC TTA GAG ATT GTG GCA ATA GCC AAG	606
Val Ile Ser Leu Leu Glu Asn Ile Leu Glu Ile Val Ala Ile Ala Lys	
60 65 70	
AAC AAG AAT CTG CAT TCA CCC ATG TAC TTT TTC ATC TGC AGC TTG GCT	654
Asn Lys Asn Leu His Ser Pro Met Tyr Phe Phe Ile Cys Ser Leu Ala	
75 80 85	
GTG GCT GAT ATG CTG GTG AGC GTT TCA AAT GGA TCA GAA ACC ATT ATC	702
Val Ala Asp Met Leu Val Ser Val Ser Asn Gly Ser Glu Thr Ile Ile	
90 95 100	
ATC ACC CTA TTA AAC CGT ACA GAT ACG GAT GCA CAG AGT TTC ACA GTG	750
Ile Thr Leu Leu Asn Arg Thr Asp Thr Asp Ala Gln Ser Phe Thr Val	
105 110 115	
AAT ATT GAT AAT GTC ATT GAC TCG GTG ATC TGT AGC TCC TTG CTT GCA	798
Asn Ile Asp Asn Val Ile Asp Ser Val Ile Cys Ser Ser Leu Leu Ala	
120 125 130 135	
TCC ATT TGC AGC CTG CTT TCA ATT GCA GTG GAC AGG TAC TTT ACT ATC	846
Ser Ile Cys Ser Leu Leu Ser Ile Ala Val Asp Arg Tyr Phe Thr Ile	
140 145 150	
TTC TAT GCT CTC CAG TAC CAT AAC ATT ATG ACA GTT AAG CGG GTT GGG	894
Phe Tyr Ala Leu Gln Tyr His Asn Ile Met Thr Val Lys Arg Val Gly	
155 160 165	
ATC AGC ATA AGT TGT ATC TGG GCA GCT TGC ACG GTT TCA GGT ATT TTG	942
Ile Ser Ile Ser Cys Ile Trp Ala Ala Cys Thr Val Ser Gly Ile Leu	
170 175 180	
TTC ATC ATT TAC TCA GAT AGT AGT GCT GTC ATC ATC TGC CTC ATC ACC	990
Phe Ile Ile Tyr Ser Asp Ser Ser Ala Val Ile Ile Cys Leu Ile Thr	
185 190 195	
ATG TTC TTC ACC ATG CTG GCT CTC ATG GCT TCT CTC TAT GTC CAC CTG	1038
Met Phe Phe Thr Met Leu Ala Leu Met Ala Ser Leu Tyr Val His Leu	
200 205 210 215	
TTC CTG ATG GCC AGG CTT CAC ATT AAG AGG ATT GCT GTC CTC CCC GGC	1086
Phe Leu Met Ala Arg Leu His Ile Lys Arg Ile Ala Val Leu Pro Gly	
220 225 230	
ACT GGT GCC ATC CGC CAA GGT GCC AAT ATG AAG GGA GCG ATT ACC TTG	1134
Thr Gly Ala Ile Arg Gln Gly Ala Asn Met Lys Gly Ala Ile Thr Leu	
235 240 245	



ACC ATC CTG ATT GGC GTC TTT GTT GTC TGC TGG GCC CCA TTC TTC CTC	1182
Thr Ile Leu Ile Gly Val Phe Val Val Cys Trp Ala Pro Phe Phe Leu	
250 255 260	
CAC TTA ATA TTC TAC ATC TCT TGT CCT CAG AAT CCA TAT TGT GTG TGC	1230
His Leu Ile Phe Tyr Ile Ser Cys Pro Gln Asn Pro Tyr Cys Val Cys	
265 270 275	
TTC ATG TCT CAC TTT AAC TTG TAT CTC ATA CTG ATC ATG TGT AAT TCA	1278
Phe Met Ser His Phe Asn Leu Tyr Leu Ile Leu Ile Met Cys Asn Ser	
280 285 290 295	
ATC ATC GAT CCT CTG ATT TAT GCA CTC CGG AGT CAA GAA CTG AGG AAA	1326
Ile Ile Asp Pro Leu Ile Tyr Ala Leu Arg Ser Gln Glu Leu Arg Lys	
300 305 310	
ACC TTC AAA GAG ATC ATC TCT TCC TAT CCC CTG GGA GGC CTT TGT GAC	1374
Thr Phe Lys Glu Ile Ile Ser Ser Tyr Pro Leu Gly Gly Leu Cys Asp	
315 320 325	
TTG TCT AGC AGA TAT TAAATGGGGA CAGAGCACGC AATATAGGAA CATCCATAAG	1429
Leu Ser Ser Arg Tyr	
330	
AGACTTTTTC ACTCTTACCC TACCTGAATA TTCTACTTCT GCAACAGCTT TCTCTTCCGT	1489
GTAGGGTACT GGTTGAGATA TCCATTGTGT AAATTTAAGC CTATGATTTT TAATGAGAAA	1549
AAATGCCCAG TCTCTGTATT ATTTCCAATC TCATGCTACT TTTTGGCCA TAAAATATGA	1609
ATCTATGTTA TAGGTTGTAG GCACTGTGGA TTTACAAAAA GAAAAGTCCT TATTAAAAGA	1669
TT	1671

## (2) INFORMATION FOR SEQ ID NO:16:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Val Asn Ser Thr His Arg Gly Met His Thr Ser Leu His Leu Trp
1 5 10 15
Asn Arg Ser Ser Tyr Arg Leu His Ser Asn Ala Ser Glu Ser Leu Gly
20 25 30

Lys Gly Tyr Ser Asp Gly Gly Cys Tyr Ala Gln Leu Phe Val Ser Pro  
                   35                                  40                                  45  
 Glu Val Phe Val Thr Leu Gly Val Ile Ser Leu Leu Glu Asn Ile Leu  
           50                                  55                                  60  
 Glu Ile Val Ala Ile Ala Lys Asn Lys Asn Leu His Ser Pro Met Tyr  
           65                                  70                                  75                                  80  
 Phe Phe Ile Cys Ser Leu Ala Val Ala Asp Met Leu Val Ser Val Ser  
                                   85                                  90                                  95  
 Asn Gly Ser Glu Thr Ile Ile Ile Thr Leu Leu Asn Arg Thr Asp Thr  
                                   100                                  105                                  110  
 Asp Ala Gln Ser Phe Thr Val Asn Ile Asp Asn Val Ile Asp Ser Val  
                   115                                  120                                  125  
 Ile Cys Ser Ser Leu Leu Ala Ser Ile Cys Ser Leu Leu Ser Ile Ala  
           130                                  135                                  140  
 Val Asp Arg Tyr Phe Thr Ile Phe Tyr Ala Leu Gln Tyr His Asn Ile  
           145                                  150                                  155                                  160  
 Met Thr Val Lys Arg Val Gly Ile Ser Ile Ser Cys Ile Trp Ala Ala  
                                   165                                  170                                  175  
 Cys Thr Val Ser Gly Ile Leu Phe Ile Ile Tyr Ser Asp Ser Ser Ala  
                                   180                                  185                                  190  
 Val Ile Ile Cys Leu Ile Thr Met Phe Phe Thr Met Leu Ala Leu Met  
                   195                                  200                                  205  
 Ala Ser Leu Tyr Val His Leu Phe Leu Met Ala Arg Leu His Ile Lys  
           210                                  215                                  220  
 Arg Ile Ala Val Leu Pro Gly Thr Gly Ala Ile Arg Gln Gly Ala Asn  
           225                                  230                                  235                                  240  
 Met Lys Gly Ala Ile Thr Leu Thr Ile Leu Ile Gly Val Phe Val Val  
                                   245                                  250                                  255  
 Cys Trp Ala Pro Phe Phe Leu His Leu Ile Phe Tyr Ile Ser Cys Pro  
                   260                                  265                                  270  
 Gln Asn Pro Tyr Cys Val Cys Phe Met Ser His Phe Asn Leu Tyr Leu  
           275                                  280                                  285  
 Ile Leu Ile Met Cys Asn Ser Ile Ile Asp Pro Leu Ile Tyr Ala Leu  
           290                                  295                                  300

Arg Ser Gln Glu Leu Arg Lys Thr Phe Lys Glu Ile Ile Ser Ser Tyr  
 305 310 315 320

Pro Leu Gly Gly Leu Cys Asp Leu Ser Ser Arg Tyr  
 325 330

## (2) INFORMATION FOR SEQ ID NO:17:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 978 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..975

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATG AAC TCC TCC TCC ACC CTG ACT GTA TTG AAT CTT ACC CTG AAC GCC	48
Met Asn Ser Ser Ser Thr Leu Thr Val Leu Asn Leu Thr Leu Asn Ala	
1 5 10 15	
TCA GAG GAT GGC ATT TTA GGA TCA AAT GTC AAG AAC AAG TCT TTG GCC	96
Ser Glu Asp Gly Ile Leu Gly Ser Asn Val Lys Asn Lys Ser Leu Ala	
20 25 30	
TGT GAA GAA ATG GGC ATT GCC GTG GAG GTG TTC CTG ACC CTG GGT CTC	144
Cys Glu Glu Met Gly Ile Ala Val Glu Val Phe Leu Thr Leu Gly Leu	
35 40 45	
GTC AGC CTC TTA GAG AAC ATC CTG GTC ATT GGG GCC ATA GTA AAG AAC	192
Val Ser Leu Leu Glu Asn Ile Leu Val Ile Gly Ala Ile Val Lys Asn	
50 55 60	
AAA AAC CTG CAC TCA CCC ATG TAC TTC TTT GTG GGC AGC TTA GCC GTG	240
Lys Asn Leu His Ser Pro Met Tyr Phe Phe Val Gly Ser Leu Ala Val	
65 70 75 80	
GCC GAC ATG CTG GTG AGC ATG TCC AAT GCC TGG GAG ACT GTC ACC ATA	288
Ala Asp Met Leu Val Ser Met Ser Asn Ala Trp Glu Thr Val Thr Ile	
85 90 95	
TAC TTG CTA AAT AAT AAA CAC CTG GTG ATA GCC GAC ACC TTT GTG CGA	336
Tyr Leu Leu Asn Asn Lys His Leu Val Ile Ala Asp Thr Phe Val Arg	
100 105 110	

CAC ATC GAC AAC GTG TTC GAC TCC ATG ATC TGC ATC TCT GTG GTG GCC	384
His Ile Asp Asn Val Phe Asp Ser Met Ile Cys Ile Ser Val Val Ala	
115 120 125	
TCG ATG TGC AGT TTG CTG GCC ATT GCG GTG GAT AGG TAC ATC ACC ATC	432
Ser Met Cys Ser Leu Leu Ala Ile Ala Val Asp Arg Tyr Ile Thr Ile	
130 135 140	
TTC TAT GCC TTG CGC TAC CAC CAC ATC ATG ACC GCG AGG CGC TCG GGG	480
Phe Tyr Ala Leu Arg Tyr His His Ile Met Thr Ala Arg Arg Ser Gly	
145 150 155 160	
GTG ATC ATC GCC TGC ATT TGG ACC TTC TGC ATA AGC TGC GGC ATT GTT	528
Val Ile Ile Ala Cys Ile Trp Thr Phe Cys Ile Ser Cys Gly Ile Val	
165 170 175	
TTC ATC ATC TAC TAT GAG TCC AAG TAT GTG ATC ATT TGC CTC ATC TCC	576
Phe Ile Ile Tyr Tyr Glu Ser Lys Tyr Val Ile Ile Cys Leu Ile Ser	
180 185 190	
ATG TTC TTC ACC ATG CTG TTC TTC ATG GTG TCT CTG TAT ATA CAC ATG	624
Met Phe Phe Thr Met Leu Phe Phe Met Val Ser Leu Tyr Ile His Met	
195 200 205	
TTC CTC CTG GCC CGG AAC CAT GTC AAG CGG ATA GCA GCT TCC CCC AGA	672
Phe Leu Leu Ala Arg Asn His Val Lys Arg Ile Ala Ala Ser Pro Arg	
210 215 220	
TAC AAC TCC GTG AGG CAA AGG ACC AGC ATG AAG GGG GCT ATT ACC CTC	720
Tyr Asn Ser Val Arg Gln Arg Thr Ser Met Lys Gly Ala Ile Thr Leu	
225 230 235 240	
ACC ATG CTA CTG GGG ATT TTC ATT GTC TGC TGG TCT CCC TTC TTT CTT	768
Thr Met Leu Leu Gly Ile Phe Ile Val Cys Trp Ser Pro Phe Phe Leu	
245 250 255	
CAC CTT ATC TTA ATG ATC TCC TGC CCT CAG AAC GTC TAC TGC TCT TGC	816
His Leu Ile Leu Met Ile Ser Cys Pro Gln Asn Val Tyr Cys Ser Cys	
260 265 270	
TTT ATG TCT TAC TTC AAC ATG TAC CTT ATA CTC ATC ATG TGC AAC TCC	864
Phe Met Ser Tyr Phe Asn Met Tyr Leu Ile Leu Ile Met Cys Asn Ser	
275 280 285	
GTG ATC GAT CCT CTC ATC TAC GCC CTC CGC AGC CAA GAG ATG CGG AGG	912
Val Ile Asp Pro Leu Ile Tyr Ala Leu Arg Ser Gln Glu Met Arg Arg	
290 295 300	
ACC TTT AAG GAG ATC GTC TGT TGT CAC GGA TTC CGG CGA CCT TGT AGG	960
Thr Phe Lys Glu Ile Val Cys Cys His Gly Phe Arg Arg Pro Cys Arg	
305 310 315 320	

CTC CTT GGC GGG TAT TAA  
 Leu Leu Gly Gly Tyr  
 325

978

## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met	Asn	Ser	Ser	Ser	Thr	Leu	Thr	Val	Leu	Asn	Leu	Thr	Leu	Asn	Ala	1	5	10	15
Ser	Glu	Asp	Gly	Ile	Leu	Gly	Ser	Asn	Val	Lys	Asn	Lys	Ser	Leu	Ala	20	25	30	
Cys	Glu	Glu	Met	Gly	Ile	Ala	Val	Glu	Val	Phe	Leu	Thr	Leu	Gly	Leu	35	40	45	
Val	Ser	Leu	Leu	Glu	Asn	Ile	Leu	Val	Ile	Gly	Ala	Ile	Val	Lys	Asn	50	55	60	
Lys	Asn	Leu	His	Ser	Pro	Met	Tyr	Phe	Phe	Val	Gly	Ser	Leu	Ala	Val	65	70	75	80
Ala	Asp	Met	Leu	Val	Ser	Met	Ser	Asn	Ala	Trp	Glu	Thr	Val	Thr	Ile	85	90	95	
Tyr	Leu	Leu	Asn	Asn	Lys	His	Leu	Val	Ile	Ala	Asp	Thr	Phe	Val	Arg	100	105	110	
His	Ile	Asp	Asn	Val	Phe	Asp	Ser	Met	Ile	Cys	Ile	Ser	Val	Val	Ala	115	120	125	
Ser	Met	Cys	Ser	Leu	Leu	Ala	Ile	Ala	Val	Asp	Arg	Tyr	Ile	Thr	Ile	130	135	140	
Phe	Tyr	Ala	Leu	Arg	Tyr	His	His	Ile	Met	Thr	Ala	Arg	Arg	Ser	Gly	145	150	155	160
Val	Ile	Ile	Ala	Cys	Ile	Trp	Thr	Phe	Cys	Ile	Ser	Cys	Gly	Ile	Val	165	170	175	

Phe Ile Ile Tyr Tyr Glu Ser Lys Tyr Val Ile Ile Cys Leu Ile Ser  
                   180                                  185                                  190  
 Met Phe Phe Thr Met Leu Phe Phe Met Val Ser Leu Tyr Ile His Met  
                   195                                  200                                  205  
 Phe Leu Leu Ala Arg Asn His Val Lys Arg Ile Ala Ala Ser Pro Arg  
                   210                                  215                                  220  
 Tyr Asn Ser Val Arg Gln Arg Thr Ser Met Lys Gly Ala Ile Thr Leu  
                   225                                  230                                  235                                  240  
 Thr Met Leu Leu Gly Ile Phe Ile Val Cys Trp Ser Pro Phe Phe Leu  
                                   245                                  250                                  255  
 His Leu Ile Leu Met Ile Ser Cys Pro Gln Asn Val Tyr Cys Ser Cys  
                                   260                                  265                                  270  
 Phe Met Ser Tyr Phe Asn Met Tyr Leu Ile Leu Ile Met Cys Asn Ser  
                   275                                  280                                  285  
 Val Ile Asp Pro Leu Ile Tyr Ala Leu Arg Ser Gln Glu Met Arg Arg  
                   290                                  295                                  300  
 Thr Phe Lys Glu Ile Val Cys Cys His Gly Phe Arg Arg Pro Cys Arg  
                   305                                  310                                  315                                  320  
 Leu Leu Gly Gly Tyr  
                                   325

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..32
- (D) OTHER INFORMATION: /function = "Degenerate  
oligonucleotide primer (antisense)"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GAATTCGACG TCACAGTATG ACGGCCATGG

30

**WHAT WE CLAIM IS:**

1. A method for characterizing a compound as an agonist of a mammalian melanocortin receptor, the method comprising the steps of:

5 (a) providing a panel comprising a first mammalian cell comprising a recombinant expression construct encoding a mammalian melanocortin receptor that is the  $\alpha$ -MSH receptor, a second mammalian cell comprising a recombinant expression construct encoding a mammalian melanocortin receptor that is the ACTH receptor, a third mammalian cell comprising a recombinant expression construct encoding a mammalian melanocortin receptor that is the MC-3 receptor, a fourth mammalian cell  
10 comprising a recombinant expression construct encoding a mammalian melanocortin receptor that is the MC-4 receptor, and a fifth mammalian cell comprising a recombinant expression construct encoding a mammalian melanocortin receptor that is the MC-5 receptor, wherein each mammalian cell expresses the melanocortin receptor encoded by the recombinant expression construct comprising the cell;

15 (b) contacting each of the cells of the panel with a test compound to be characterized as an agonist of a mammalian melanocortin receptor;

(c) detecting binding of the test compound to each of the mammalian melanocortin receptors by assaying for a metabolite produced in the cells that bind the compound.  
20

2. The method of claim 1, wherein the metabolite detected in subpart (c) is cyclic AMP.

25 3. The method of claim 1, each of the cells further comprising a recombinant expression construct encoding a cyclic AMP responsive element (CRE) transcription factor binding site operatively linked to a nucleic acid sequence encoding a protein capable of producing a detectable metabolite.

30 4. The method of claim 3, wherein the nucleic acid sequence encodes  $\beta$ -galactosidase.

5. The method of claim 3, wherein the recombinant expression construct is pCRE/ $\beta$ -galactosidase.

5 6. The method of claim 3, wherein the detectable metabolite produced by the protein encoded by the recombinant expression construct is produced by binding of the test compound to the mammalian melanocortin receptor encoded by each of the cells of the panel.

10 7. A method for characterizing a compound as an antagonist of a mammalian melanocortin receptor, the method comprising the steps of:

(a) providing a panel comprising a first mammalian cell comprising a recombinant expression construct encoding a mammalian melanocortin receptor that is the  $\alpha$ -MSH receptor, a second mammalian cell comprising a recombinant expression construct encoding a mammalian melanocortin receptor that is the ACTH receptor, a  
15 third mammalian cell comprising a recombinant expression construct encoding a mammalian melanocortin receptor that is the MC-3 receptor, a fourth mammalian cell comprising a recombinant expression construct encoding a mammalian melanocortin receptor that is the MC-4 receptor, and a fifth mammalian cell comprising a recombinant expression construct encoding a mammalian melanocortin receptor that is the MC-5  
20 receptor, wherein each mammalian cell expresses the melanocortin receptor encoded by the recombinant expression construct comprising the cell;

(b) contacting each of the cells of the panel with an agonist of the mammalian melanocortin receptor in an amount sufficient to produce a detectable amount of a metabolite produced in the cells that bind the agonist, in the presence or  
25 absence of a test compound to be characterized as an antagonist of a mammalian melanocortin receptor;

(c) detecting the amount of the metabolite produced in each cell in the panel in the presence of the test compound with the amount of the metabolite produced in each cell in the panel in the absence.

30

8. The method of claim 7, wherein the metabolite detected in subpart (c) is cyclic AMP.



9. The method of claim 7, each of the cells further comprising a recombinant expression construct encoding a cyclic AMP responsive element (CRE) transcription factor binding site operatively linked to a nucleic acid sequence encoding a protein capable of producing a detectable metabolite.

5

10. The method of claim 9, wherein the nucleic acid sequence encodes  $\beta$ -galactosidase.

11. The method of claim 9, wherein the recombinant expression construct is pCRE/ $\beta$ -galactosidase.

10

12. The method of claim 9, wherein the detectable metabolite produced by the protein encoded by the recombinant expression construct is produced by binding of the test compound to the mammalian melanocortin receptor encoded by each of the cells of the panel.

15

13. The method of claim 1 wherein the test compound is an agonist of the MC-3 mammalian melanocortin receptor.

14. The method of claim 1 wherein the test compound is an agonist of the MC-4 mammalian melanocortin receptor.

20

15. The method of claim 3 wherein the test compound is an agonist of the MC-3 mammalian melanocortin receptor.

25

16. The method of claim 3 wherein the test compound is an agonist of the MC-4 mammalian melanocortin receptor.

17. The method of claim 7 wherein the test compound is an antagonist of the MC-3 mammalian melanocortin receptor.

30

18. The method of claim 7 wherein the test compound is an antagonist of the MC-4 mammalian melanocortin receptor.

5 19. The method of claim 9 wherein the test compound is an antagonist of the MC-3 mammalian melanocortin receptor.

20. The method of claim 9 wherein the test compound is an antagonist of the MC-4 mammalian melanocortin receptor.

10 21. A mammalian melanocortin MC-3 receptor agonist according to claims 13 or 15.

22. A mammalian melanocortin MC-4 receptor agonist according to claims 14 or 16.

15 23. A mammalian melanocortin MC-3 receptor antagonist according to claims 17 or 19.

20 24. A mammalian melanocortin MC-4 receptor antagonist according to claims 18 or 20.

25 25. A method of inhibiting feeding behavior in an animal, the method comprising administering an effective amount of a mammalian melanocortin MC-3 or MC-4 receptor agonist according to claim 21.

26. A method of stimulating feeding behavior in an animal, the method comprising administering an effective amount of a mammalian melanocortin MC-3 or MC-4 receptor antagonist according to claim 24.

30 27. A method for characterizing a mammalian melanocortin MC-3 or MC-4 receptor agonist as an inhibitor of feeding behavior in an animal, the method comprising:

(a) providing food to an animal that has been deprived of food for at least 12 hours with or without administering to the animal a mammalian melanocortin MC-3 or MC-4 receptor agonist according to claim 25; and

(b) comparing the amount of food eaten by the animal with and without administration of the mammalian melanocortin MC-3 or MC-4 receptor agonist.

28. A method for characterizing a mammalian melanocortin MC-3 or MC-4 receptor antagonist as a stimulator of feeding behavior in an animal, the method comprising:

(a) providing food to an animal that has not been otherwise deprived of food for at least 12 hours, with or without administering to the animal a mammalian melanocortin MC-3 or MC-4 receptor antagonist according to claim 26 immediately prior to the onset of darkness or nighttime; and

(b) comparing the amount of food eaten by the animal with and without administration of the mammalian melanocortin MC-3 or MC-4 receptor antagonist.

29. A mammalian melanocortin MC-3 or MC-4 receptor agonist having the general formula:

A-B-C-D-E-F-G-amide

wherein A is Leu, Ile, Nle, Met, or substituted analogues thereof;

B is Asp, Glu, or substituted analogues thereof;

C is His or substituted analogues thereof;

D is D-Phe, D-Tyr or substituted analogues thereof;

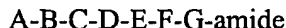
E is Arg, Lys, homoArg, homoLys, or substituted analogues thereof;

F is Trp or substituted analogues thereof;

G is Lys, homoLys or substituted analogues thereof;

and wherein the peptide is cyclized by the formation of an amide bond between the side chain carboxyl group of the Asp or Glu residue at position B in the peptide, and the side chain amino group of the Lys or homoLys residue at position G.

30. A mammalian melanocortin MC-3 or MC-4 receptor antagonist having the general formula:



wherein A is Leu, Ile, Nle, Met, or substituted analogues thereof;

5 B is Asp, Glu or substituted analogues thereof;

C is His or substituted analogues thereof;

D is D-Nal or substituted analogues thereof;

E is Arg, Lys, homoArg, homoLys or substituted analogues thereof;

F is Trp or substituted analogues thereof;

10 G is Lys, homoLys or substituted analogues thereof;

and wherein the peptide is cyclized by the formation of an amide bond between the side chain carboxyl group of the Asp or Glu residue at position B in the peptide, and the side chain amino group of the Lys or homoLys residue at position G.

15 31. A biological screening panel for determining the receptor agonist/antagonist profile of a test compound, the panel comprising a first mammalian cell comprising a recombinant expression construct encoding a mammalian melanocortin receptor that is the  $\alpha$ -MSH receptor, a second mammalian cell comprising a recombinant expression construct encoding a mammalian melanocortin receptor that is the ACTH receptor, a third mammalian cell comprising a recombinant expression construct encoding a mammalian melanocortin receptor that is the MC-3 receptor, a fourth mammalian cell comprising a recombinant expression construct encoding a mammalian melanocortin receptor that is the MC-4 receptor, and a fifth mammalian cell comprising a recombinant expression construct encoding a mammalian melanocortin receptor that is the MC-5 receptor, wherein each mammalian cell expresses the melanocortin receptor encoded by the recombinant expression construct comprising the cell.

20

25

FIG. 1A

TTCCTGACAA	GACT	ATG	TCC	ACT	CAG	GAG	CCC	CAG	AAG	AGT	CTT	CTG	GGT			50
		Met	Ser	Thr	Gln	Glu	Pro	Gln	Lys	Ser	Leu	Leu	Gly			
		1				5					10					
TCT	CTC	AAC	TCC	AAT	GCC	ACC	TCT	CAC	CTT	GGA	CTG	GCC	ACC	AAC	CAG	98
Ser	Leu	Asn	Ser	Asn	Ala	Thr	Ser	His	Leu	Gly	Leu	Ala	Thr	Asn	Gln	
	15					20					25					
TCA	GAG	CCT	TGG	TGC	CTG	TAT	GTG	TCC	ATC	CCA	GAT	GGC	CTC	TTC	CTC	146
Ser	Glu	Pro	Trp	Cys	Leu	Tyr	Val	Ser	Ile	Pro	Asp	Gly	Leu	Phe	Leu	
	30					35					40					
AGC	CTA	GGG	CTG	GTG	AGT	CTG	GTG	GAG	AAT	GTG	CTG	GTT	GTG	ATA	GCC	194
Ser	Leu	Gly	Leu	Val	Ser	Leu	Val	Glu	Asn	Val	Leu	Val	Val	Ile	Ala	
	45				50				55						60	
ATC	ACC	AAA	AAC	CGC	AAC	CTG	CAC	TCG	CCC	ATG	TAT	TAC	TTC	ATC	TGC	242
Ile	Thr	Lys	Asn	Arg	Asn	Leu	His	Ser	Pro	Met	Tyr	Tyr	Phe	Ile	Cys	
				65					70					75		
TGC	CTG	GCC	CTG	TCT	GAC	CTG	ATG	GTA	AGT	GTC	AGC	ATC	GTG	CTG	GAG	290
Cys	Leu	Ala	Leu	Ser	Asp	Leu	Met	Val	Ser	Val	Ser	Ile	Val	Leu	Glu	
		80						85					90			
ACT	ACT	ATC	ATC	CTG	CTG	CTG	GAG	GTG	GGC	ATC	CTG	GTG	GCC	AGA	GTG	338
Thr	Thr	Ile	Ile	Leu	Leu	Leu	Glu	Val	Gly	Ile	Leu	Val	Ala	Arg	Val	
		95					100					105				
GCT	TTG	GTG	CAG	CAG	CTG	GAC	AAC	CTC	ATT	GAC	GTG	CTC	ATC	TGT	GGC	386
Ala	Leu	Val	Gln	Gln	Leu	Asp	Asn	Leu	Ile	Asp	Val	Leu	Ile	Cys	Gly	
	110					115					120					
TCC	ATG	GTG	TCC	AGT	CTC	TGC	TTC	CTG	GGC	ATC	ATT	GCT	ATA	GAC	CGC	434
Ser	Met	Val	Ser	Ser	Leu	Cys	Phe	Leu	Gly	Ile	Ile	Ala	Ile	Asp	Arg	
	125				130				135					140		
TAC	ATC	TCC	ATC	TTC	TAT	GCG	CTG	CGT	TAT	CAC	AGC	ATC	GTG	ACG	CTG	482
Tyr	Ile	Ser	Ile	Phe	Tyr	Ala	Leu	Arg	Tyr	His	Ser	Ile	Val	Thr	Leu	
				145				150					155			
CCC	AGA	GCA	CGA	CGG	GCT	GTC	GTG	GGC	ATC	TGG	ATG	GTC	AGC	ATC	GTC	530
Pro	Arg	Ala	Arg	Arg	Ala	Val	Val	Gly	Ile	Trp	Met	Val	Ser	Ile	Val	
		160						165					170			

1146

FIG. 1B

TCC AGC ACC CTC TTT ATC ACC TAC TAC AAG CAC ACA GCC GTT CTG CTC	578
Ser Ser Thr Leu Phe Ile Thr Tyr Tyr Lys His Thr Ala Val Leu Leu	
175 180 185	
TGC CTC GTC ACT TTC TTT CTA GCC ATG CTG GCA CTC ATG GCG ATT CTG	626
Cys Leu Val Thr Phe Phe Leu Ala Met Leu Ala Leu Met Ala Ile Leu	
190 195 200	
TAT GCC CAC ATG TTC ACG AGA GCG TGC CAG CAC GTC CAG GGC ATT GCC	674
Tyr Ala His Met Phe Thr Arg Ala Cys Gln His Val Gln Gly Ile Ala	
205 210 215 220	
CAG CTC CAC AAA AGG CGG CGG TCC ATC CGC CAA GGC TTC TGC CTC AAG	722
Gln Leu His Lys Arg Arg Ser Ile Arg Gln Gly Phe Cys Leu Lys	
225 230 235	
GGT GCT GCC ACC CTT ACT ATC CTT CTG GGG ATT TTC TTC CTG TGC TGG	770
Gly Ala Ala Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp	
240 245 250	
GGC CCC TTC TTC CTG CAT CTC TTG CTC ATC GTC CTC TGC CCT CAG CAC	818
Gly Pro Phe Phe Leu His Leu Leu Leu Ile Val Leu Cys Pro Gln His	
255 260 265	
CCC ACC TGC AGC TGC ATC TTC AAG AAC TTC AAC CTC TTC CTC CTC CTC	866
Pro Thr Cys Ser Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Leu Leu	
270 275 280	
ATC GTC CTC AGC TCC ACT GTT GAC CCC CTC ATC TAT GCT TTC CGC AGC	914
Ile Val Leu Ser Ser Thr Val Asp Pro Leu Ile Tyr Ala Phe Arg Ser	
285 290 295 300	
CAG GAG CTC CGC ATG ACA CTC AAG GAG GTG CTG CTG TGC TCC TGG	959
Gln Glu Leu Arg Met Thr Leu Lys Glu Val Leu Leu Cys Ser Trp	
305 310 315	
TGATCAGAGG GCGCTGGGCA GAGGGTGACA GTGATATCCA GTGGCCTGCA TCTGTGAGAC	1019
CACAGGTACT CATCCCTTCC TGATCTCCAT TTGTCTAAGG GTCGACAGGA TGAGCTTTAA	1079
AATAGAAACC CAGAGTGCCT GGGGCCAGGA GAAAGGGTAA CTGTGACTGC AGGGCTCACC	1139
CAGGGCAGCT ACGGGAAGTG GAGGAGACAG GGATGGGAAC TCTAGCCCTG AGCAAGGGTC	1199
AGACCACAGG CTCCTGAAGA GCTTCACCTC TCCCCACCTA CAGGCAACTC CTGCTCAAGC	1259
C	1260

2/46

FIG. 2A

CCCCCATGTG GCCGCCCTCA ATGGAGGGCT CTGAGAACGA CTTTAAAAAC GCAGAGAAAA	60
AGCTCCATTC TTCCAGACC TCAGCGCAGC CCTGGCCCAG GAAGGGAGGA GACAGAGGCC	120
AGGACGGTCC AGAGGTGTCTG AAATGTCCTG GGAACCTGAG CAGCAGCCAC CAGGGAAGAG	180
GCAGGGAGGG AGCTGAGGAC CAGGCTTGGT TGTGAGAATC CCTGAGCCCA GCGGTTGAT	240
GCCAGGAGGT GTCTGGACTG GCTGGGCCAT GCCTGGGCTG ACCTGTCCAG CCAGGGAGAG	300
GGTGTGAGGG CAGATCTGGG GGTGCCCAGA TGGAAGGAGG CAGGCATGGG GACACCCAAG	360
GCCCCCTGGC AGCACCATGA ACTAAGCAGG ACACCTGGAG GGAAGAAGT GTGGGGACCT	420
GGAGGCCTCC AACGACTCCT TCCTGCTTCC TGGACAGGAC T ATG GCT GTG CAG	473
Met Ala Val Gln	
1	
GGA TCC CAG AGA AGA CTT CTG GGC TCC CTC AAC TCC ACC CCC ACA GCC	521
Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser Thr Pro Thr Ala	
5 10 15 20	
ATC CCC CAG CTG GGG CTG GCT GCC AAC CAG ACA GGA GCC CGG TGC CTG	569
Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly Ala Arg Cys Leu	
25 30 35	
GAG GTG TCC ATC TCT GAC GGG CTC TTC CTC AGC CTG GGG CTG GTG AGC	617
Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu Gly Leu Val Ser	
40 45 50	
TTG GTG GAG AAC GCG CTG GTG GTG GCC ACC ATC GCC AAG AAC CGG AAC	665
Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala Lys Asn Arg Asn	
55 60 65	
CTG CAC TCA CCC ATG TAC TGC TTC ATC TGC TGC CTG GCC TTG TCG GAC	713
Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu Ala Leu Ser Asp	
70 75 80	
CTG CTG GTG AGC GGG ACG AAC GTG CTG GAG ACG GCC GTC ATC CTC CTG	761
Leu Leu Val Ser Gly Thr Asn Val Leu Glu Thr Ala Val Ile Leu Leu	
85 90 95 100	
CTG GAG GCC GGT GCA CTG GTG GCC CGG GCT GCG GTG CTG CAG CAG CTG	809
Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val Leu Gln Gln Leu	
105 110 115	
GAC AAT GTC ATT GAC GTG ATC ACC TGC AGC TCC ATG CTG TCC AGC CTC	857
Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met Leu Ser Ser Leu	
120 125 130	
TGC TTC CTG GGC GCC ATC GCC GTG GAC CGC TAC ATC TCC ATC TTC TAC	905
Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile Ser Ile Phe Tyr	
135 140 145	
GCA CTG CGC TAC CAC AGC ATC GTG ACC CTG CCG CGG GCG CCG CGA GCC	953
Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg Ala Pro Arg Ala	
150 155 160	

3/46

FIG. 2B

GTT GCG GCC ATC TGG GTG GCC AGT GTC GTC TTC AGC ACG CTC TTC ATC Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser Thr Leu Phe Ile 165 170 175 180	1001
GCC TAC TAC GAC CAC GTG GCC GTC CTG CTG TGC CTC GTG GTC TTC TTC Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu Val Val Phe Phe 185 190 195	1049
CTG GCT ATG CTG GTG CTC ATG GCC GTG CTG TAC GTC CAC ATG CTG GCC Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val His Met Leu Ala 200 205 210	1097
CGG GCC TGC CAG CAC GCC CAG GGC ATC GCC CGG CTC CAC AAG AGG CAG Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu His Lys Arg Gln 215 220 225	1145
CGC CCG GTC CAC CAG GGC TTT GGC CTT AAA GGC GCT GTC ACC CTC ACC Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala Val Thr Leu Thr 230 235 240	1193
ATC CTG CTG GGC ATT TTC TTC CTC TGC TGG GGC CCC TTC TTC CTG CAT Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro Phe Phe Leu His 245 250 255 260	1241
CTC ACA CTC ATC GTC CTC TGC CCC GAG CAC CCC ACG TGC GGC TGC ATC Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr Cys Gly Cys Ile 265 270 275	1289
TTC AAG AAC TTC AAC CTC TTT CTC GCC CTC ATC ATC TGC AAT GCC ATC Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile Cys Asn Ala Ile 280 285 290	1337
ATC GAC CCC CTC ATC TAC GCC TTC CAC AGC CAG GAG CTC CGC AGG ACG Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu Leu Arg Arg Thr 295 300 305	1385
CTC AAG GAG GTG CTG ACA TGC TCC TGG TGAGCGCGGT GCACGCGCTT Leu Lys Glu Val Leu Thr Cys Ser Trp 310 315	1432
TAAGTGTGCT GGGCAGAGGG AGGTGGTGAT ATTGTGGTCT GGTTCCTGTG TGACCCTGGG	1492
CAGTTTCCTTA CCTCCCTGGT CCCCCTTTGT CAAAGAGGAT GGAATAAATG ATCTCTGAAA	1552
GTGTTGAAGC GCGGACCCCTT CTGGGCAGGG AGGGGTCTCTG CAAAACTCCA GGCAGGACTT	1612
CTCACCAGCA GTCGTGGGAA C	1633

4/46



FIG. 3A

ACAACACTTT ATATATATTT TTATAAATGT AAGGGGTACA AAGGTGCCAT TTTGTTACAT	60
GGATATAACCG TGTAGTGGTG AAGCCTGGGC TTTTAGTGTA TCTGTCATCA GAATAACATA	120
CGTGTTACCC ATAGGAATTT CTCATCACCC GCCCCTCCA CCCTTCGAGT CTCCAATGTC	180
CATTCCACAC TCTATATCCA CGTGATGCA TATAGCTCCA CATATAAGTG AGAACATGTA	240
GTATTTGACT TCCTCTTCT GAGTTATTTC ACTTTGATAA TGGCCTCCAC TTCCATCCAT	300
GTTGCTGCAA AAGACATGAC CTTATTCTTT TTGATAGCTG GGGAGTACTC CATTGTGTAT	360
ATGTACCACA TTTCTTTATC CATTACCCCA TTGAGAACAC TTAGTTGATT CCATATCTTT	420
GCTATTGTCA CTAGTGCTGC AATAAACATA CATGTGCAGG CTCCTTCTAA TATACTGATT	480
TATATTTTAT GGAGAGAGAT AGAGTTCTTA GCGAGTGTGC TGTTTATTTC TAGTGTACTT	540
GCAACTAATA TTCTGTATAC TCCCTTTAGG TGATTGGAGA TTAACTTAG ATCTCCAGCA	600
AGTGCTACAA GAAGAAAAGA TCCTGAAGAA TCAATCAAGT TTCCGTGAAG TCAAGTCCAA	660
GTAACATCCC CGCCTTAACC ACAAGCAGGA GAA ATG AAG CAC ATT ATC AAC TCG	714
Met Lys His Ile Ile Asn Ser	
1 5	
TAT GAA AAC ATC AAC AAC ACA GCA AGA AAT AAT TCC GAC TGT CCT CGT	762
Tyr Glu Asn Ile Asn Asn Thr Ala Arg Asn Asn Ser Asp Cys Pro Arg	
10 15 20	
GTG GTT TTG CCG GAG GAG ATA TTT TTC ACA ATT TCC ATT GTT GGA GTT	810
Val Val Leu Pro Glu Glu Ile Phe Phe Thr Ile Ser Ile Val Gly Val	
25 30 35	
TTG GAG AAT CTG ATC GTC CTG CTG GCT GTG TTC AAG AAT AAG AAT CTC	858
Leu Glu Asn Leu Ile Val Leu Leu Ala Val Phe Lys Asn Lys Asn Leu	
40 45 50 55	
CAG GCA CCC ATG TAC TTT TTC ATC TGT AGC TTG GCC ATA TCT GAT ATG	906
Gln Ala Pro Met Tyr Phe Phe Ile Cys Ser Leu Ala Ile Ser Asp Met	
60 65 70	
CTG GGC AGC CTA TAT AAG ATC TTG GAA AAT ATC CTG ATC ATA TTG AGA	954
Leu Gly Ser Leu Tyr Lys Ile Leu Glu Asn Ile Leu Ile Ile Leu Arg	
75 80 85	
AAC ATG GGC TAT CTC AAG CCA CGT GGC AGT TTT GAA ACC ACA GCC GAT	1002
Asn Met Gly Tyr Leu Lys Pro Arg Gly Ser Phe Glu Thr Thr Ala Asp	
90 95 100	
GAC ATC ATC GAC TCC CTG TTT GTC CTC TCC CTG CTT GGC TCC ATC TTC	1050
Asp Ile Ile Asp Ser Leu Phe Val Leu Ser Leu Leu Gly Ser Ile Phe	
105 110 115	

5/46

FIG. 3B

AGC CTG TCT GTG ATT GCT GCG GAC CGC TAC ATC ACC ATC TTC CAC GCA	1098
Ser Leu Ser Val Ile Ala Ala Asp Arg Tyr Ile Thr Ile Phe His Ala	
120 125 130 135	
CTG CGG TAC CAC AGC ATC GTG ACC ATG CGC CGC ACT GTG GTG GTG CTT	1146
Leu Arg Tyr His Ser Ile Val Thr Met Arg Arg Thr Val Val Val Leu	
140 145 150	
ACG GTC ATC TGG ACG TTC TGC ACG GGG ACT GGC ATC ACC ATG GTG ATC	1194
Thr Val Ile Trp Thr Phe Cys Thr Gly Thr Gly Ile Thr Met Val Ile	
155 160 165	
TTC TCC CAT CAT GTG CCC ACA GTG ATC ACC TTC ACG TCG CTG TTC CCG	1242
Phe Ser His His Val Pro Thr Val Ile Thr Phe Thr Ser Leu Phe Pro	
170 175 180	
CTG ATG CTG GTC TTC ATC CTG TGC CTC TAT GTG CAC ATG TTC CTG CTG	1290
Leu Met Leu Val Phe Ile Leu Cys Leu Tyr Val His Met Phe Leu Leu	
185 190 195	
GCT CGA TCC CAC ACC AGG AAG ATC TCC ACC CTC CCC AGA GCC AAC ATG	1338
Ala Arg Ser His Thr Arg Lys Ile Ser Thr Leu Pro Arg Ala Asn Met	
200 205 210 215	
AAA GGG GCC ATC ACA CTG ACC ATC CTG CTC GGG GTC TTC ATC TTC TGC	1386
Lys Gly Ala Ile Thr Leu Thr Ile Leu Leu Gly Val Phe Ile Phe Cys	
220 225 230	
TGG GCC CCC TTT GTG CTT CAT GTC CTC TTG ATG ACA TTC TGC CCA AGT	1434
Trp Ala Pro Phe Val Leu His Val Leu Leu Met Thr Phe Cys Pro Ser	
235 240 245	
AAC CCC TAC TGC GCC TGC TAC ATG TCT CTC TTC CAG GTG AAC GGC ATG	1482
Asn Pro Tyr Cys Ala Cys Tyr Met Ser Leu Phe Gln Val Asn Gly Met	
250 255 260	
TTG ATC ATG TGC AAT GCC GTC ATT GAC CCC TTC ATA TAT GCC TTC CGG	1530
Leu Ile Met Cys Asn Ala Val Ile Asp Pro Phe Ile Tyr Ala Phe Arg	
265 270 275	
AGC CCA GAG CTC AGG GAC GCA TTC AAA AAG ATG ATC TTC TGC AGC AGG	1578
Ser Pro Glu Leu Arg Asp Ala Phe Lys Lys Met Ile Phe Cys Ser Arg	
280 285 290 295	
TAC TGG TAGAATGGCT GATCCCTGGT TTTAGAATCC ATGGGAATAA CGTTGCCAAG	1634
Tyr Trp	
TGCCAGAATA GTGTAACATT CCAACAAATG CCAGTGCTCC TCACTGGCCT TCCTTCCCTA	1694
ATGGATGCAA GGATGACCCA CCAGCTAGTG TTTCTGAATA CTATGGCCAG GAACAGTCTA	1754
TTGTAGGGGC AACTCTATTT GTGACTGGAC AGATAAAACG TGTAGTAAAA GAAGGATAGA	1814
ATACAAAGTA TTAGGTACAA AAGTAATTAG GTTTGCATTA CTTATGACAA ATGCATTACT	1874
TTTGCAACCAA TCTAGTAAAA CAGCAATAAA AATTCAAGGG CTTTGGGCTA AGGCAAAGAC	1934
TTGCTTTTCCT GTGGACATTA ACAAGCCAGT TCTGAGGCGG CCTTTCCAGG TGGAGGCCAT	1994
TGCAGCCAAT TTCAGAGT	2012

6/46

FIG. 4A

GGGGCCAGAA AGTTCCTGCT TCAGAGCAGA AGATCTTCAG CAAGAACTAC AAAGAAGAAA	60
AGATTCTGGA GAATCAATCA AGTTTCCTGT CAAGTTCAG TAACGTTTCT GTCTTAACTG	120
CACACAGGAA AG ATG AAA CAC ATT CTC AAT CTG TAT GAA AAC ATC AAC	168
Met Lys His Ile Leu Asn Leu Tyr Glu Asn Ile Asn	
1 5 10	
AGT ACA GCA AGA AAT AAC TCA GAC TGT CCT GCT GTG ATT TTG CCA GAA	216
Ser Thr Ala Arg Asn Asn Ser Asp Cys Pro Ala Val Ile Leu Pro Glu	
15 20 25	
GAG ATA TTT TTC ACA GTA TCC ATT GTT GGG GTT TTG GAG AAC CTG ATG	264
Glu Ile Phe Phe Thr Val Ser Ile Val Gly Val Leu Glu Asn Leu Met	
30 35 40	
GTC CTT CTG GCT GTG GCC AAG AAT AAG AGT CTT CAG TCG CCC ATG TAC	312
Val Leu Leu Ala Val Ala Lys Asn Lys Ser Leu Gln Ser Pro Met Tyr	
45 50 55 60	
TTT TTC ATC TGC AGC TTG GCT ATT TCC GAT ATG CTG GGG AGC CTG TAC	360
Phe Phe Ile Cys Ser Leu Ala Ile Ser Asp Met Leu Gly Ser Leu Tyr	
65 70 75	
AAG ATT TTG GAA AAC GTT CTG ATC ATG TTC AAA AAC ATG GGT TAC CTC	408
Lys Ile Leu Glu Asn Val Leu Ile Met Phe Lys Asn Met Gly Tyr Leu	
80 85 90	
GAG CCT CGA GGC AGT TTT GAA AGC ACA GCA GAT GAT GTG GTG GAC TCC	456
Glu Pro Arg Gly Ser Phe Glu Ser Thr Ala Asp Asp Val Val Asp Ser	
95 100 105	
CTG TTC ATC CTC TCC CTT CTC GGC TCC ATC TGC AGC CTG TCT GTG ATT	504
Leu Phe Ile Leu Ser Leu Leu Gly Ser Ile Cys Ser Leu Ser Val Ile	
110 115 120	
GCC GCT GAC CGC TAC ATC ACA ATC TTC CAC GCT CTG CAG TAC CAC CGC	552
Ala Ala Asp Arg Tyr Ile Thr Ile Phe His Ala Leu Gln Tyr His Arg	
125 130 135 140	
ATC ATG ACC CCC GCA CCG TGC CCT CGT CAT CTG ACG GTC CTC TGG GCA	600
Ile Met Thr Pro Ala Pro Cys Pro Arg His Leu Thr Val Leu Trp Ala	
145 150 155	
GGC TGC ACA GGC AGT GGC ATT ACC ATC GTG ACC TTC TCC CAT CAC GTC	648
Gly Cys Thr Gly Ser Gly Ile Thr Ile Val Thr Phe Ser His His Val	
160 165 170	
CCC ACA GTG ATC GCC TTC ACA GCG CTG TTC CCG CTG ATG CTG GCC TTC	696
Pro Thr Val Ile Ala Phe Thr Ala Leu Phe Pro Leu Met Leu Ala Phe	
175 180 185	
ATC CTG TGC CTC TAC GTG CAC ATG TTC CTG CTG GCC CGC TCC CAC ACC	744
Ile Leu Cys Leu Tyr Val His Met Phe Leu Leu Ala Arg Ser His Thr	
190 195 200	
AGG AGG ACC CCC TCC CTT CCC AAA GCC AAC ATG AGA GGG GCC GTC ACA	792
Arg Arg Thr Pro Ser Leu Pro Lys Ala Asn Met Arg Gly Ala Val Thr	
205 210 215 220	

7/46

FIG. 4B

CTG ACT GTC CTG CTC GGG GTC TTC ATT TTC TGT TGG GCA CCC TTT GTC Leu Thr Val Leu Leu Gly Val Phe Ile Phe Cys Trp Ala Pro Phe Val 225 230 235	840
CTT CAT GTC CTC TTG ATG ACA TTC TGC CCA GCT GAC CCC TAC TGT GCC Leu His Val Leu Leu Met Thr Phe Cys Pro Ala Asp Pro Tyr Cys Ala 240 245 250	888
TGC TAC ATG TCC CTC TTC CAG GTG AAT GGT GTG TTG ATC ATG TGT AAT Cys Tyr Met Ser Leu Phe Gln Val Asn Gly Val Leu Ile Met Cys Asn 255 260 265	936
GCC ATC ATC GAC CCC TTC ATA TAT GCC TTT CGG AGC CCA GAG CTC AGG Ala Ile Ile Asp Pro Phe Ile Tyr Ala Phe Arg Ser Pro Glu Leu Arg 270 275 280	984
GTC GCA TTC AAA AAG ATG GTT ATC TGC AAC TGT TAC CAG TAGAATGATT Val Ala Phe Lys Lys Met Val Ile Cys Asn Cys Tyr Gln 285 290 295	1033
GGTCCCTGAT TTTAGGAGCC ACAGGGATAT ACTGTCAGGG ACAGAGTAGC GTGACAGACC	1093
AACAACACTA GGA CT	1108

8/46

FIG. 5A

GGCTGTA	ACT	GTAGCA	ACCG	GTGTTGGG	TG	GGGATG	AAGAA	GAGACC	AGAG	AGAGGG	60
TCAGAGC	GCAC	AGGGGAT	GAG	ACAGGCT	GGT	CAGAGT	CTGC	ACTGAT	TGTT	GGAGAC	120
AGGAAAG	TTT	TTTCTAT	GTC	TCCAAC	CTCC	CCCTCT	CTCC	CCGTTT	CTCT	CTGGAG	180
TAAAATC	TAG	ACTGGAC	CAGC	ATCCACA	AAGA	GAAGCAC	CTA	GAAGAAG	ATT	TTTTTT	240
AGCAGCT	TGC	TCAGGAC	CCCT	GCAGGAG	CTG	CAGCCG	GAAC	TGGTCCC	GCC	GATAAC	297
ATG AAC	TCT TCC	TGC TGC	CCG TCC	TCC TCT	TAT CCG	ACG CTG	CCT AAC	345			
Met Asn	Ser Ser	Cys Cys	Pro Ser	Ser Ser	Ser Tyr	Pro Thr	Leu Pro	Asn			
1		5		10		15					
CTC TCC	CAG CAC	CCT GCA	GCC CCC	TCT GCC	AGC AAC	CGG AGT	GGC AGT	393			
Leu Ser	Gln His	Pro Ala	Ala Pro	Ser Ala	Ser Asn	Arg Ser	Gly Ser				
	20		25		30						
GGG TTC	TGC GAG	CAG GTT	TTC ATC	AAG CCA	GAG GTC	TTC CTG	GCA CTG	441			
Gly Phe	Cys Glu	Gln Val	Phe Ile	Lys Pro	Glu Val	Phe Leu	Ala Leu				
	35		40		45						
GGC ATC	GTC AGT	CTG ATG	GAA AAC	ATC CTG	GTG ATC	CTG GCT	GTG GTG	489			
Gly Ile	Val Ser	Leu Met	Glu Asn	Ile Leu	Val Ile	Leu Ala	Val Val				
	50		55		60						
AGG AAC	GGC AAC	CTG CAC	TCC CCC	ATG TAC	TTC TTC	CTG CTG	AGC CTG	537			
Arg Asn	Gly Asn	Leu His	Ser Pro	Met Tyr	Phe Phe	Leu Leu	Ser Leu				
	65		70		75		80				
CTG CAG	GCC GAC	ATG CTG	GTG AGC	CTG TCC	AAC TCC	CTG GAG	ACC ATC	585			
Leu Gln	Ala Asp	Met Leu	Val Ser	Leu Ser	Asn Ser	Leu Glu	Thr Ile				
		85		90		95					
ATG ATC	GTG GTT	ATC AAC	AGC GAC	TCC CTG	ACC TTG	GAG GAC	CAA TTC	633			
Met Ile	Val Val	Ile Asn	Ser Asp	Ser Leu	Thr Leu	Glu Asp	Gln Phe				
	100		105		110						
ATC CAG	CAC ATG	GAC AAC	ATC TTC	GAC TCT	ATG ATC	TGC ATC	TCC CTG	681			
Ile Gln	His Met	Asp Asn	Ile Phe	Asp Ser	Met Ile	Cys Ile	Ser Leu				
	115		120		125						
GTG GCC	TCC ATC	TGC AAC	CTC CTG	GCC ATC	GCC GTG	GAC AGG	TAC GTC	729			
Val Ala	Ser Ile	Cys Asn	Leu Leu	Ala Ile	Ala Val	Asp Arg	Tyr Val				
	130		135		140						
ACC ATC	TTC TAT	GCC CTC	CGT TAC	CAC AGC	ATC ATG	ACG GTT	AGG AAA	777			
Thr Ile	Phe Tyr	Ala Leu	Arg Tyr	His Ser	Ile Met	Thr Val	Arg Lys				
	145		150		155		160				
GCC CTC	TCC TTG	ATC GTG	GCC ATC	TGG GTC	TGC TGT	GGC ATC	TGC GGC	825			
Ala Leu	Ser Leu	Ile Val	Ala Ile	Trp Val	Cys Cys	Gly Ile	Cys Gly				
	165		170		175						
GTG ATG	TTC ATC	GTC TAC	TCC GAG	AGC AAG	ATG GTC	ATC GTG	TGC CTC	873			
Val Met	Phe Ile	Val Tyr	Ser Glu	Ser Lys	Met Val	Ile Val	Cys Leu				
	180		185		190						

9/46

FIG. 5B

ATC ACC ATG TTC TTC GCC ATG GTG CTC CTC ATG GGC ACC CTG TAC ATC Ile Thr Met Phe Phe Ala Met Val Leu Leu Met Gly Thr Leu Tyr Ile 195 200 205	921
CAC ATG TTC CTC TTC GCC AGG CTG CAC GTC CAG CGC ATC GCG GCA CTG His Met Phe Leu Phe Ala Arg Leu His Val Gln Arg Ile Ala Ala Leu 210 215 220	969
CCA CCT GCT GAC GGG GTA GCC CCG CAG CAG CAC TCG TGC ATG AAG GGG Pro Pro Ala Asp Gly Val Ala Pro Gln Gln His Ser Cys Met Lys Gly 225 230 235 240	1017
GCC GTC ACC ATC ACC ATC CTG CTG GGG GTT TTC ATC TTC TGC TGG GCG Ala Val Thr Ile Ile Leu Leu Gly Val Phe Ile Phe Cys Trp Ala 245 250 255	1065
CCT TTC TTC CTC CAC CTG GTC CTC ATC ATC ACC TGC CCC ACC AAC CCC Pro Phe Phe Leu His Leu Val Leu Ile Ile Thr Cys Pro Thr Asn Pro 260 265 270	1113
TAC TGC ATC TGC TAC ACG GCG CAC TTC AAC ACC TAC CTG GTT CTC ATC Tyr Cys Ile Cys Tyr Thr Ala His Phe Asn Thr Tyr Leu Val Leu Ile 275 280 285	1161
ATG TGC AAC TCT GTC ATC GAC CCC CTC ATC TAC GCC TTC CGC AGC CTG Met Cys Asn Ser Val Ile Asp Pro Leu Ile Tyr Ala Phe Arg Ser Leu 290 295 300	1209
GAG CTG CGA AAC ACC TTC AAG GAG ATT CTC TGC GGT TGC AAT GGC ATG Glu Leu Arg Asn Thr Phe Lys Glu Ile Leu Cys Gly Cys Asn Gly Met 305 310 315 320	1257
AAC GTG GGC TAGGAACCCC CGAGGAGGTG TTCCACGGCT AGCCAAGAGA Asn Val Gly	1306
GAAAAGCAAT GCTCAGGTGA GACACAGAAG GG	1338

10/46

FIG. 6A

AGCTTCCGAG AGGCAGCCGA TGTGAGCATG TGCGCACAGA TTCGTCTCCC AATGGCATGG	60
CAGCTTCAAG GAAAATTATT TTGAACAGAC TTGAATGCAT AAGATTAAAG TTAAAGCAGA	120
AGTGAGAACA AGAAAGCAAA GAGCAGACTC TTTCAACTGA GAATGAATAT TTTGAAGCCC	180
AAGATTTTAA AGTGATGATG ATTAGAGTCG TACCTAAAAG AGACTAAAAA CTCCATGTCA	240
AGCTCTGGAC TTGTGACATT TACTCACAGC AGGCATGGCA ATTTTAGCCT CACAACTTTC	300
AGACAGATAA AGACTTGGAG GAAATAACTG AGACGACTCC CTGACCCAGG AGGTTAAATC	360
AATTCAGGGG GACACTGGAA TTCTCCTGCC AGC ATG GTG AAC TCC ACC CAC CGT	414
Met Val Asn Ser Thr His Arg	
1 5	
GGG ATG CAC ACT TCT CTG CAC CTC TGG AAC CGC AGC AGT TAC AGA CTG	462
Gly Met His Thr Ser Leu His Leu Trp Asn Arg Ser Ser Tyr Arg Leu	
10 15 20	
CAC AGC AAT GCC AGT GAG TCC CTT GGA AAA GGC TAC TCT GAT GGA GGG	510
His Ser Asn Ala Ser Glu Ser Leu Gly Lys Gly Tyr Ser Asp Gly Gly	
25 30 35	
TGC TAC GAG CAA CTT TTT GTC TCT CCT GAG GTG TTT GTG ACT CTG GGT	558
Cys Tyr Glu Gln Leu Phe Val Ser Pro Glu Val Phe Val Thr Leu Gly	
40 45 50 55	
GTG ATC AGC TTG TTG GAG AAT ATC TTA GTG ATT GTG GCA ATA GCC AAG	606
Val Ile Ser Leu Leu Glu Asn Ile Leu Val Ile Val Ala Ile Ala Lys	
60 65 70	
AAC AAG AAT CTG CAT TCA CCC ATG TAC TTT TTC ATC TGC AGC TTG GCT	654
Asn Lys Asn Leu His Ser Pro Met Tyr Phe Phe Ile Cys Ser Leu Ala	
75 80 85	
GTG GCT GAT ATG CTG GTG AGC GTT TCA AAT GGA TCA GAA ACC ATT ATC	702
Val Ala Asp Met Leu Val Ser Val Ser Asn Gly Ser Glu Thr Ile Ile	
90 95 100	
ATC ACC CTA TTA AAC AGT ACA GAT ACG GAT GCA CAG AGT TTC ACA GTG	750
Ile Thr Leu Leu Asn Ser Thr Asp Thr Asp Ala Gln Ser Phe Thr Val	
105 110 115	
AAT ATT GAT AAT GTC ATT GAC TCG GTG ATC TGT AGC TCC TTG CTT GCA	798
Asn Ile Asp Asn Val Ile Asp Ser Val Ile Cys Ser Ser Leu Leu Ala	
120 125 130 135	
TCC ATT TGC AGC CTG CTT TCA ATT GCA GTG GAC AGG TAC TTT ACT ATC	846
Ser Ile Cys Ser Leu Leu Ser Ile Ala Val Asp Arg Tyr Phe Thr Ile	
140 145 150	
TTC TAT GCT CTC CAG TAC CAT AAC ATT ATG ACA GTT AAG CGG GTT GGG	894
Phe Tyr Ala Leu Gln Tyr His Asn Ile Met Thr Val Lys Arg Val Gly	
155 160 165	
ATC AGC ATA AGT TGT ATC TGG GCA GCT TGC ACG GTT TCA GGC ATT TTG	942
Ile Ser Ile Ser Cys Ile Trp Ala Ala Cys Thr Val Ser Gly Ile Leu	
170 175 180	

11/46

FIG. 6B

TTC ATC ATT TAC TCA GAT AGT AGT GCT GTC ATC ATC TGC CTC ATC ACC Phe Ile Ile Tyr Ser Asp Ser Ser Ala Val Ile Ile Cys Leu Ile Thr 185 190 195	990
ATG TTC TTC ACC ATG CTG GCT CTC ATG GCT TCT CTC TAT GTC CAC CTG Met Phe Phe Thr Met Leu Ala Leu Met Ala Ser Leu Tyr Val His Leu 200 205 210 215	1038
TTC CTG ATG GCC AGG CTT CAC ATT AAG AGG ATT GCT GTC CTC CCC GGC Phe Leu Met Ala Arg Leu His Ile Lys Arg Ile Ala Val Leu Pro Gly 220 225 230	1086
ACT GGT GCC ATC CGC CAA GGT GCC AAT ATG AAG GGA GCG ATT ACC TTG Thr Gly Ala Ile Arg Gln Gly Ala Asn Met Lys Gly Ala Ile Thr Leu 235 240 245	1134
ACC ATC CTG ATT GGC GTC TTT GTT GTC TGC TGG GCC CCA TTC TTC CTC Thr Ile Leu Ile Gly Val Phe Val Val Cys Trp Ala Pro Phe Phe Leu 250 255 260	1182
CAC TTA ATA TTC TAC ATC TCT TGT CCT CAG AAT CCA TAT TGT GTG TGC His Leu Ile Phe Tyr Ile Ser Cys Pro Gln Asn Pro Tyr Cys Val Cys 265 270 275	1230
TTC ATG TCT CAC TTT AAC TTG TAT CTC ATA CTG ATC ATG TGT AAT TCA Phe Met Ser His Phe Asn Leu Tyr Leu Ile Leu Ile Met Cys Asn Ser 280 285 290 295	1278
ATC ATC GAT CCT CTG ATT TAT GCA CTC CGG AGT CAA GAA CTG AGG AAA Ile Ile Asp Pro Leu Ile Tyr Ala Leu Arg Ser Gln Glu Leu Arg Lys 300 305 310	1326
ACC TTC AAA GAG ATC ATC TCT TCC TAT CCC CTG GGA GGC CTT TGT GAC Thr Phe Lys Glu Ile Ile Ser Ser Tyr Pro Leu Gly Gly Leu Cys Asp 315 320 325	1374
TTG TCT AGC AGA TAT TAAATGGGGA CAGAGCACGC AATATAGGAA CATCCATAAG Leu Ser Ser Arg Tyr 330	1429
AGACTTTTTC ACTCTTACCC TACCTGAATA TTCTACTTCT GCAACAGCTT TCTCTCCGT	1489
GTAGGGTACT GGTTGAGATA TCCATTGTGT AAATTTAAGC CTATGATTTT TAATGAGAAA	1549
AAATGCCAG TCTCTGTATT ATTTCCAATC TCATGCTACT TTTTGGCCA TAAAATATGA	1609
ATCTATGTTA TAGGTTGTAG GCACTGTGGA TTTACAAAAA GAAAAGTCCT TATTAAAAGC	1669
TT	1671

12/46



FIG. 7A

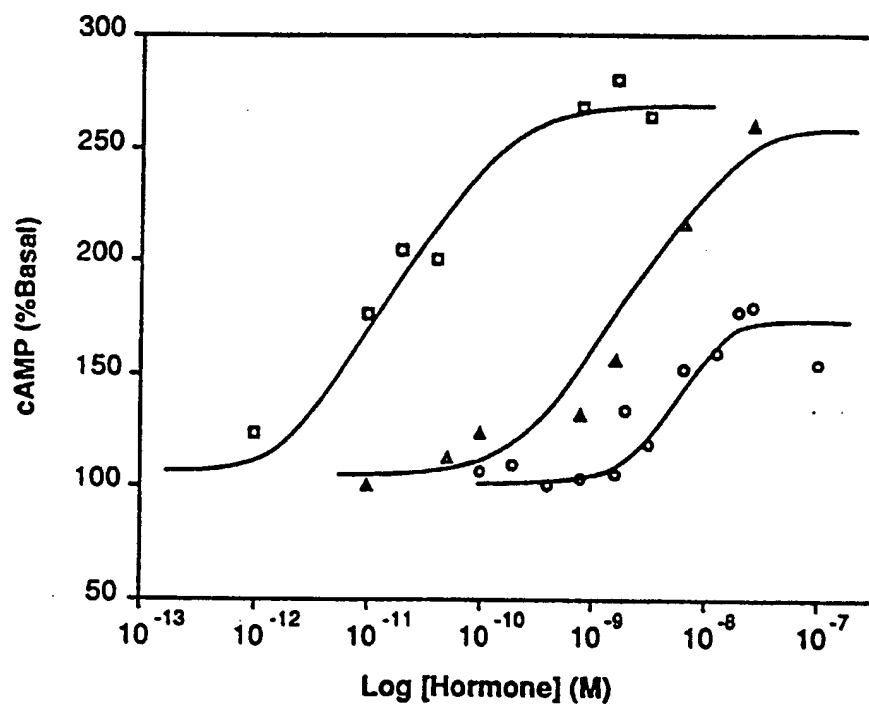
ATG AAC TCC TCC TCC ACC CTG ACT GTA TTG AAT CTT ACC CTG AAC GCC Met Asn Ser Ser Ser Thr Leu Thr Val Leu Asn Leu Thr Leu Asn Ala 1 5 10 15	48
TCA GAG GAT GGC ATT TTA GGA TCA AAT GTC AAG AAC AAG TCT TTG GCC Ser Glu Asp Gly Ile Leu Gly Ser Asn Val Lys Asn Lys Ser Leu Ala 20 25 30	96
TGT GAA GAA ATG GGC ATT GCC GTG GAG GTG TTC CTG ACC CTG GGT CTC Cys Glu Met Gly Ile Ala Val Glu Val Phe Leu Thr Leu Gly Leu 35 40 45	144
GTC AGC CTC TTA GAG AAC ATC CTG GTC ATT GGG GCC ATA GTA AAG AAC Val Ser Leu Leu Glu Asn Ile Leu Val Ile Gly Ala Ile Val Lys Asn 50 55 60	192
AAA AAC CTG CAC TCA CCC ATG TAC TTC TTT GTG GGC AGC TTA GCC GTG Lys Asn Leu His Ser Pro Met Tyr Phe Phe Val Gly Ser Leu Ala Val 65 70 75 80	240
GCC GAC ATG CTG GTG AGC ATG TCC AAT GCC TGG GAG ACT GTC ACC ATA Ala Asp Met Leu Val Ser Met Ser Asn Ala Trp Glu Thr Val Thr Ile 85 90 95	288
TAC TTG CTA AAT AAT AAA CAC CTG GTG ATA GCC GAC ACC TTT GTG CGA Tyr Leu Leu Asn Asn Lys His Leu Val Ile Ala Asp Thr Phe Val Arg 100 105 110	336
CAC ATC GAC AAC GTG TTC GAC TCC ATG ATC TGC ATC TCT GTG GTG GCC His Ile Asp Asn Val Phe Asp Ser Met Ile Cys Ile Ser Val Val Ala 115 120 125	384
TCG ATG TGC AGT TTG CTG GCC ATT GCG GTG GAT AGG TAC ATC ACC ATC Ser Met Cys Ser Leu Leu Ala Ile Ala Val Asp Arg Tyr Ile Thr Ile 130 135 140	432
TTC TAT GCC TTG CGC TAC CAC CAC ATC ATG ACC GCG AGG CGC TCG GGG Phe Tyr Ala Leu Arg Tyr His His Ile Met Thr Ala Arg Arg Ser Gly 145 150 155 160	480
GTG ATC ATC GCC TGC ATT TGG ACC TTC TGC ATA AGC TGC GGC ATT GTT Val Ile Ile Ala Cys Ile Trp Thr Phe Cys Ile Ser Cys Gly Ile Val 165 170 175	528
TTC ATC ATC TAC TAT GAG TCC AAG TAT GTG ATC ATT TGC CTC ATC TCC Phe Ile Ile Tyr Tyr Glu Ser Lys Tyr Val Ile Ile Cys Leu Ile Ser 180 185 190	576
ATG TTC TTC ACC ATG CTG TTC TTC ATG GTG TCT CTG TAT ATA CAC ATG Met Phe Phe Thr Met Leu Phe Phe Met Val Ser Leu Tyr Ile His Met 195 200 205	624
TTC CTC CTG GCC CGG AAC CAT GTC AAG CGG ATA GCA GCT TCC CCC AGA Phe Leu Leu Ala Arg Asn His Val Lys Arg Ile Ala Ala Ser Pro Arg 210 215 220	672
TAC AAC TCC GTG AGG CAA AGG ACC AGC ATG AAG GGG GCT ATT ACC CTC Tyr Asn Ser Val Arg Gln Arg Thr Ser Met Lys Gly Ala Ile Thr Leu 225 230 235 240	720

13/46

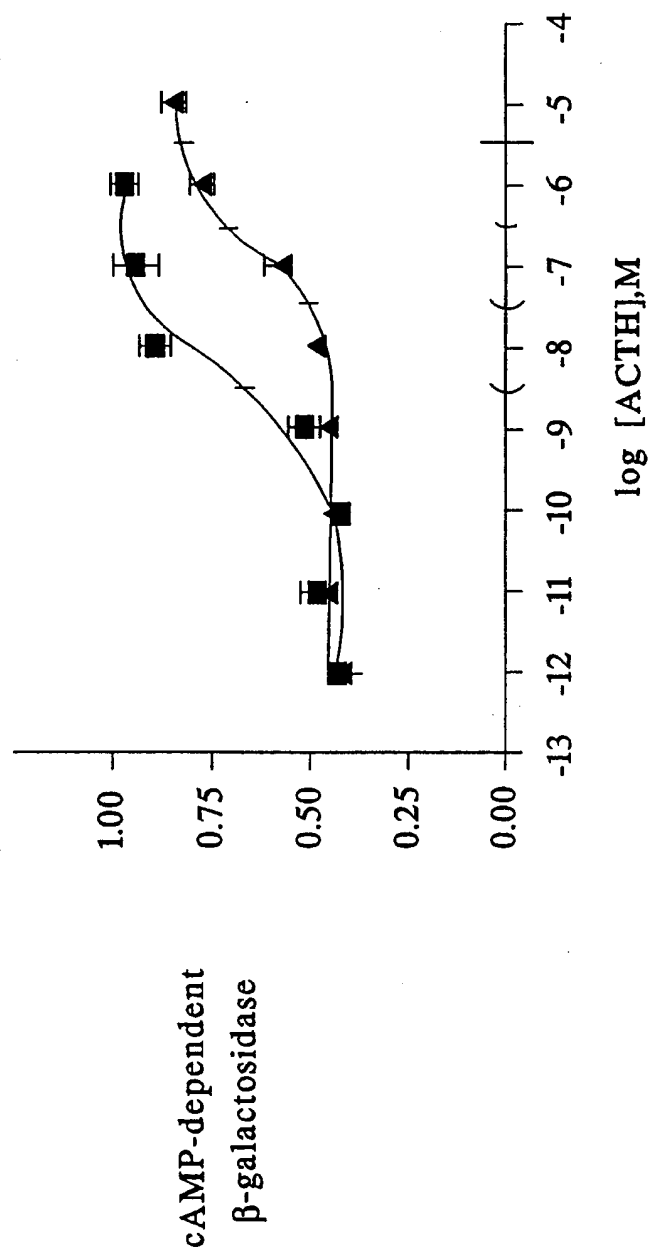
FIG. 7B

ACC ATG CTA CTG GGG ATT TTC ATT GTC TGC TGG TCT CCC TTC TTT CTT	768
Thr Met Leu Leu Gly Ile Phe Ile Val Cys Trp Ser Pro Phe Phe Leu	
245 250 255	
CAC CTT ATC TTA ATG ATC TCC TGC CCT CAG AAC GTC TAC TGC TCT TGC	816
His Leu Ile Leu Met Ile Ser Cys Pro Gln Asn Val Tyr Cys Ser Cys	
260 265 270	
TTT ATG TCT TAC TTC AAC ATG TAC CTT ATA CTC ATC ATG TGC AAC TCC	864
Phe Met Ser Tyr Phe Asn Met Tyr Leu Ile Leu Ile Met Cys Asn Ser	
275 280 285	
GTG ATC GAT CCT CTC ATC TAC GCC CTC CGC AGC CAA GAG ATG CGG AGG	912
Val Ile Asp Pro Leu Ile Tyr Ala Leu Arg Ser Gln Glu Met Arg Arg	
290 295 300	
ACC TTT AAG GAG ATC GTC TGT TGT CAC GGA TTC CGG CGA CCT TGT AGG	960
Thr Phe Lys Glu Ile Val Cys Cys His Gly Phe Arg Arg Pro Cys Arg	
305 310 315 320	
CTC CTT GGC GGG TAT TAA	978
Leu Leu Gly Gly Tyr *	
325	

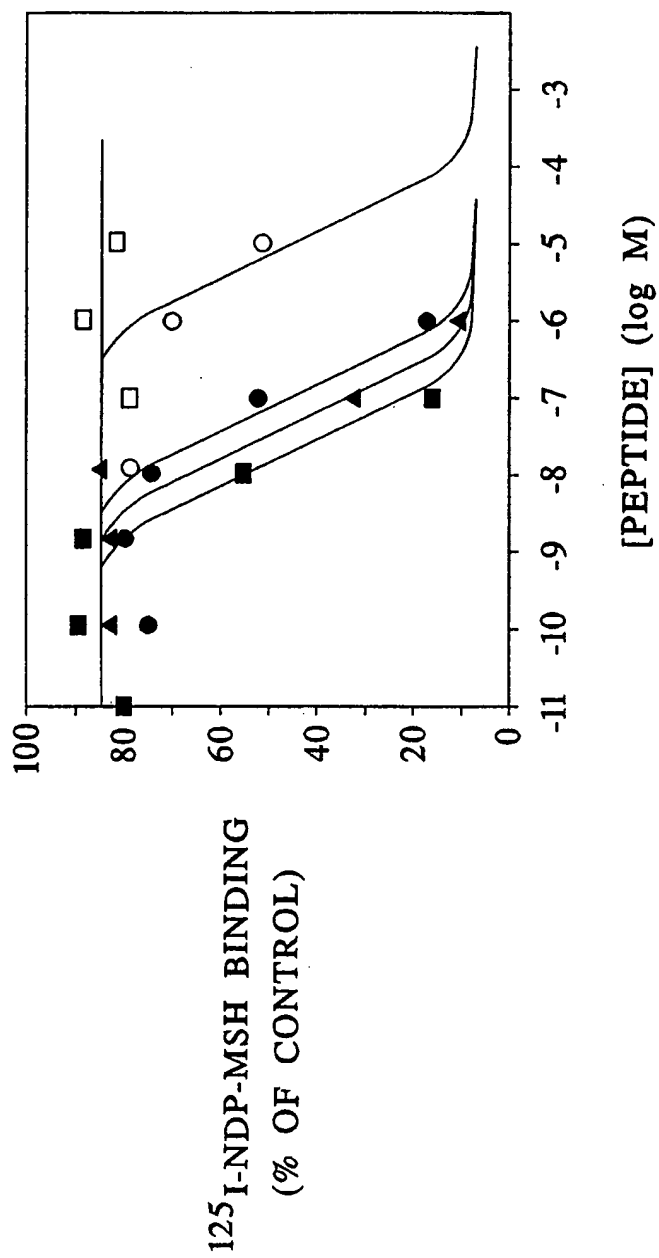
14/46

FIG. 8

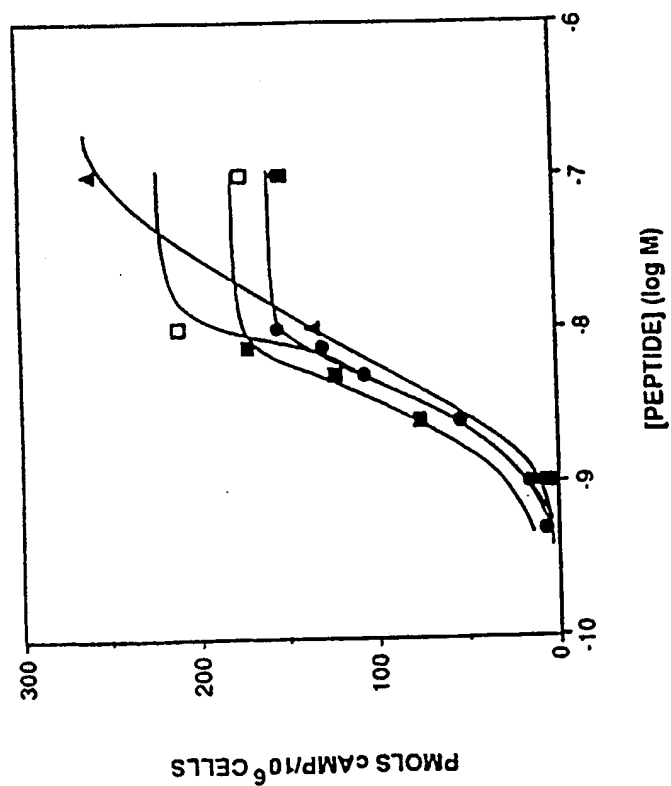
15/46

FIG. 9

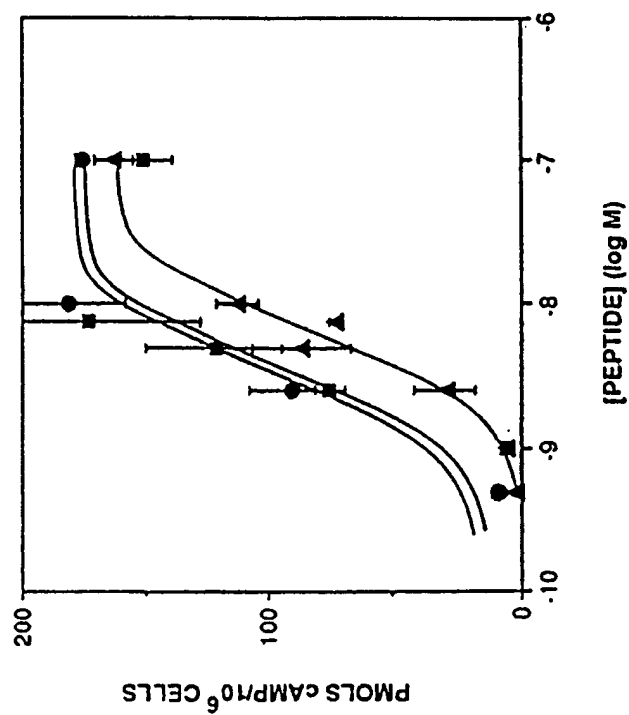
16/46

FIG. 10

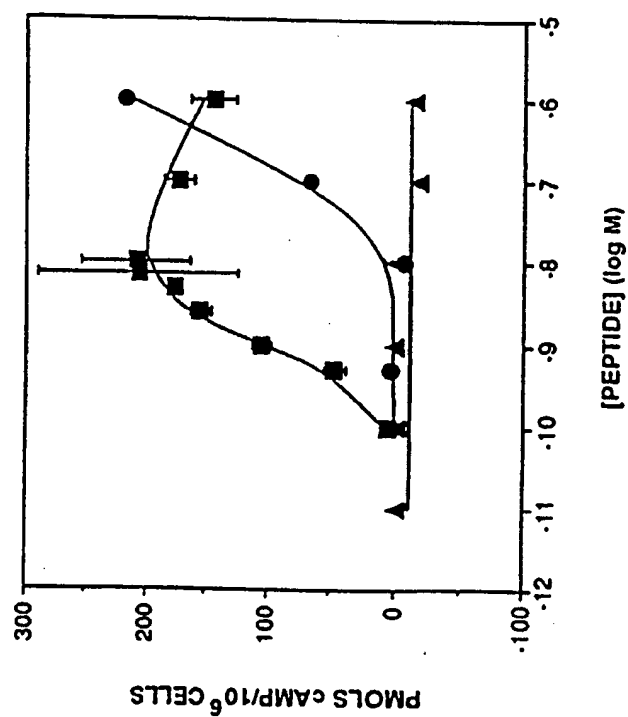
17/46

FIG. 11A

18/46

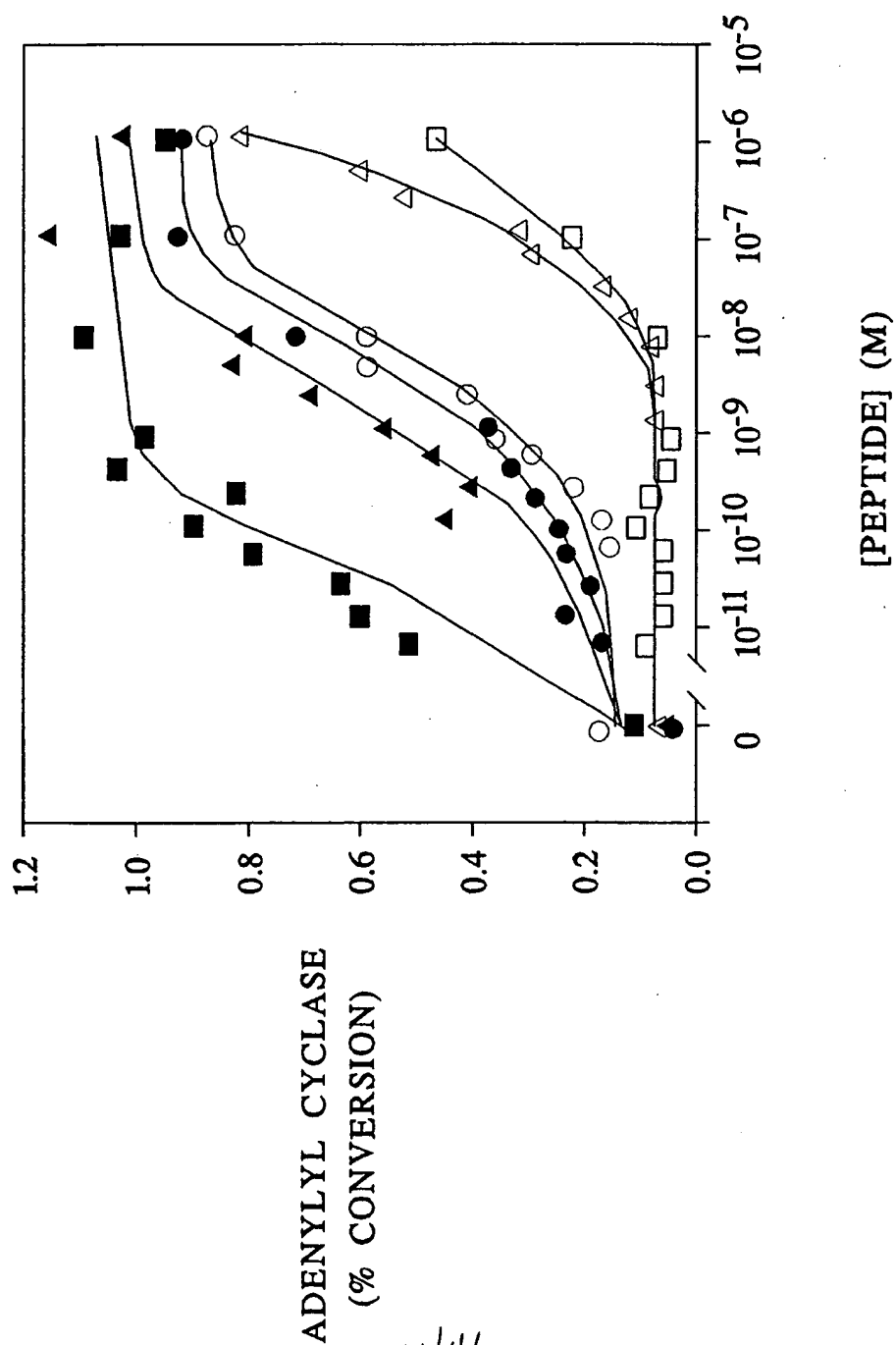
FIG. 11B

19/46

FIG. 11C

20/46

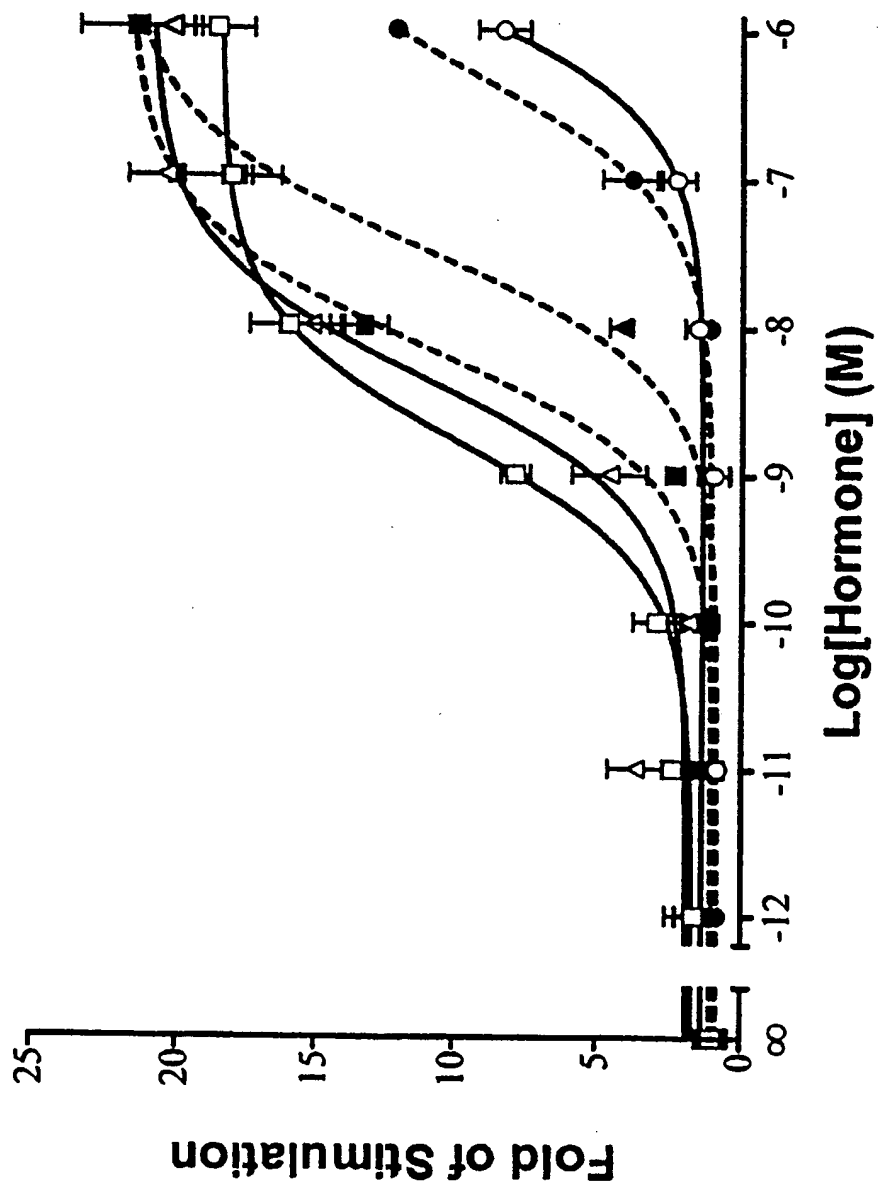


FIG. 12

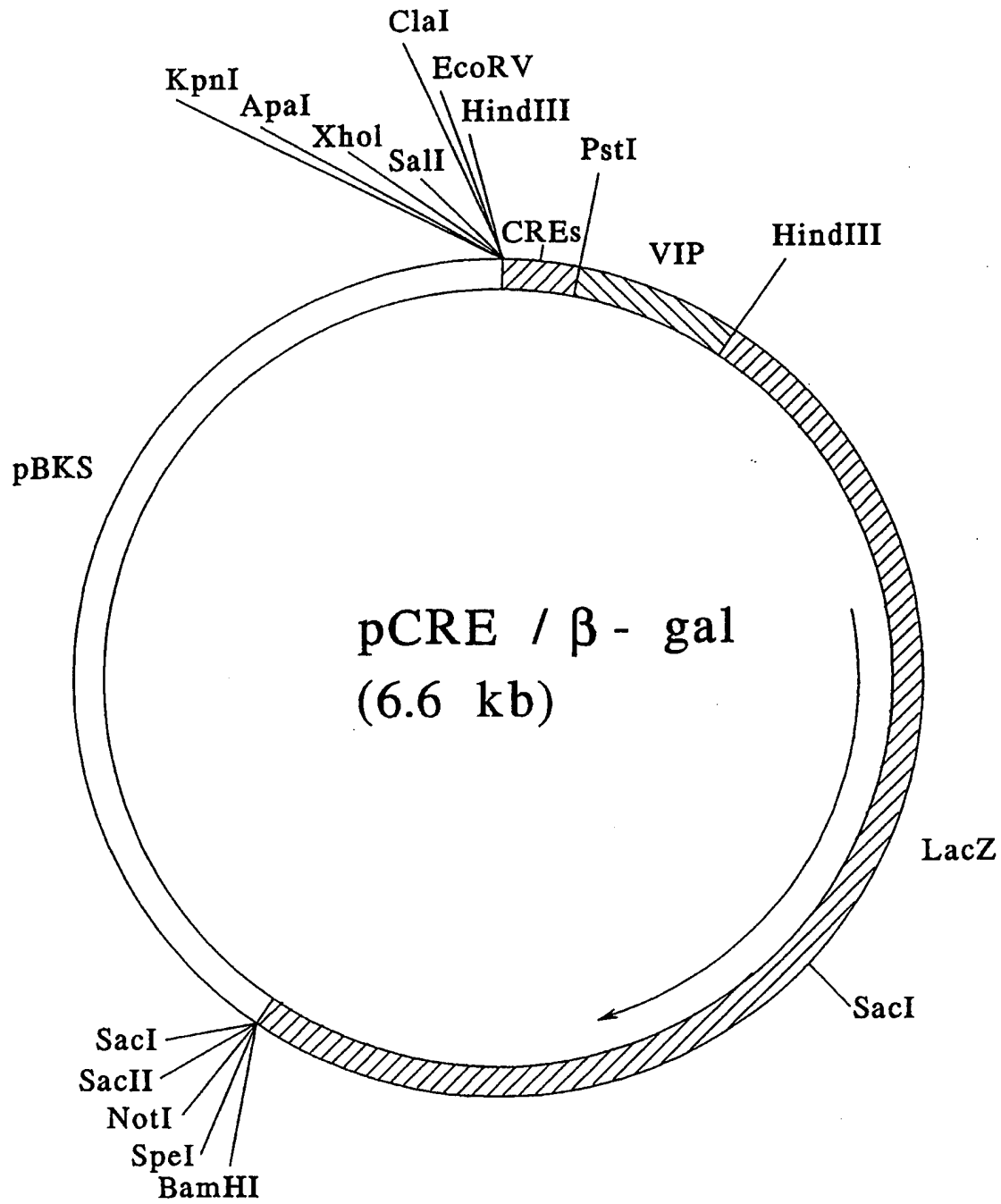
ADENYLYL CYCLASE  
(% CONVERSION)

[PEPTIDE] (M)

21/46

FIG. 13

22/46

FIG. 14

23/46

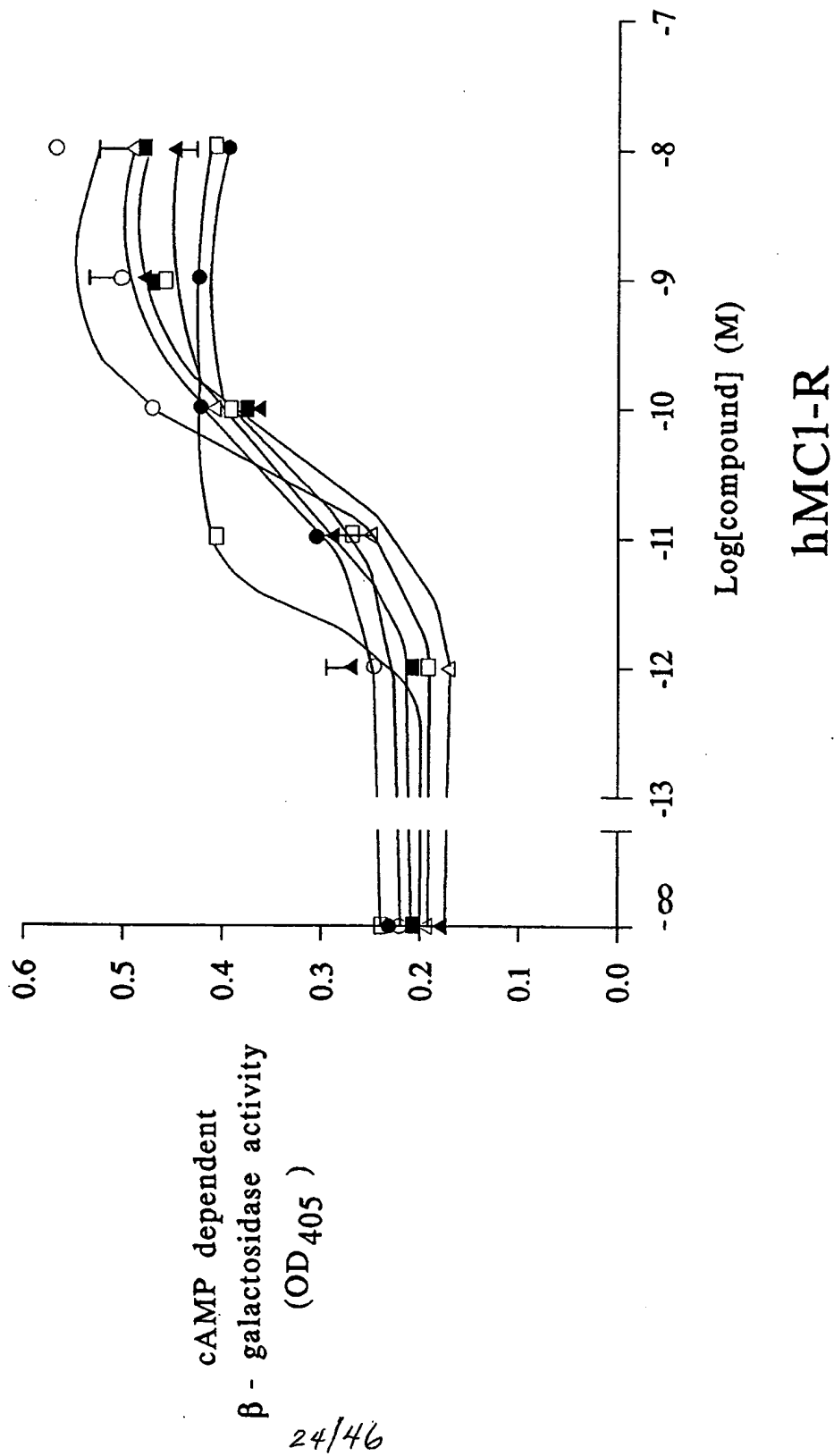
FIG. 15A

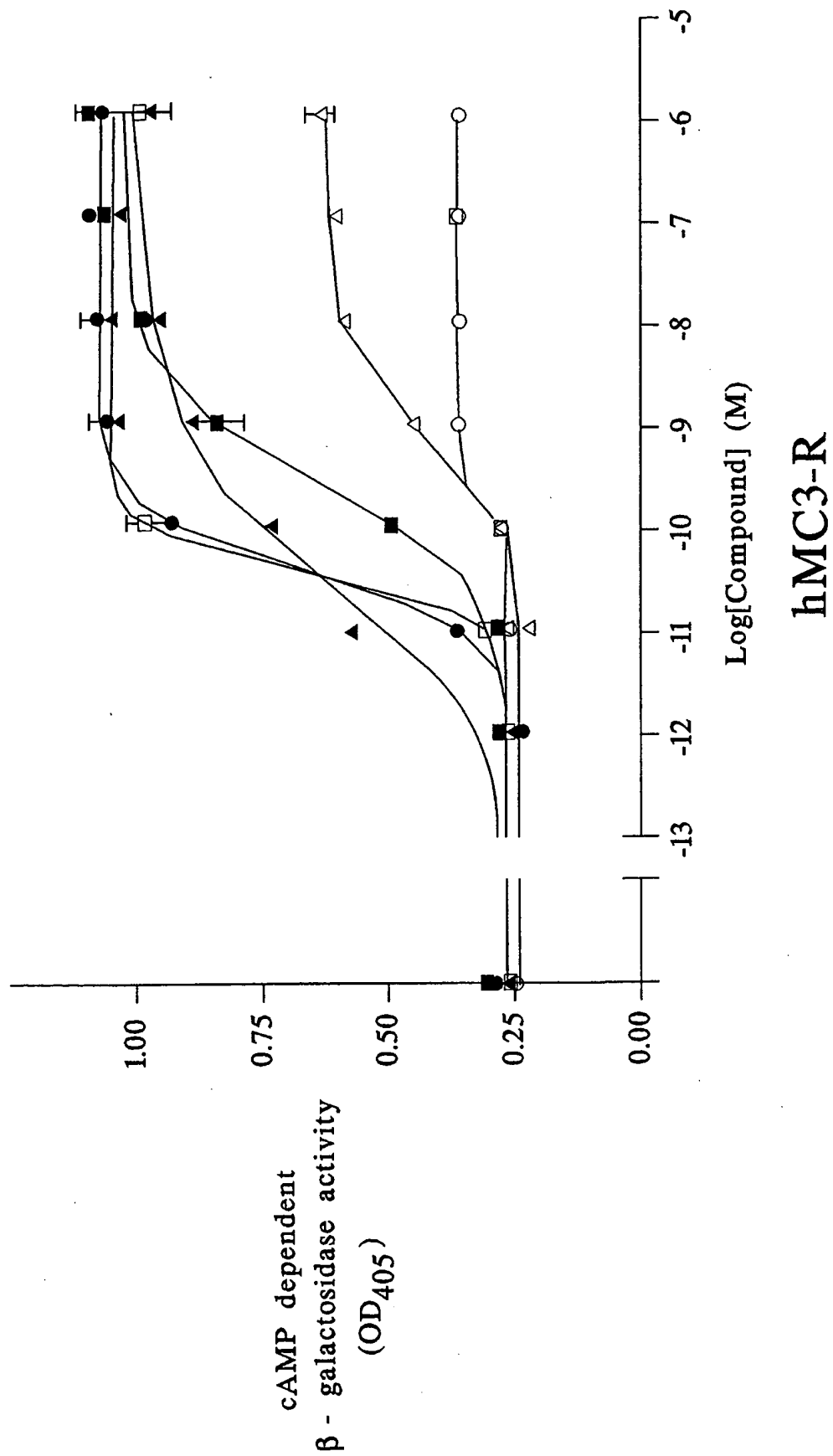
FIG. 15B

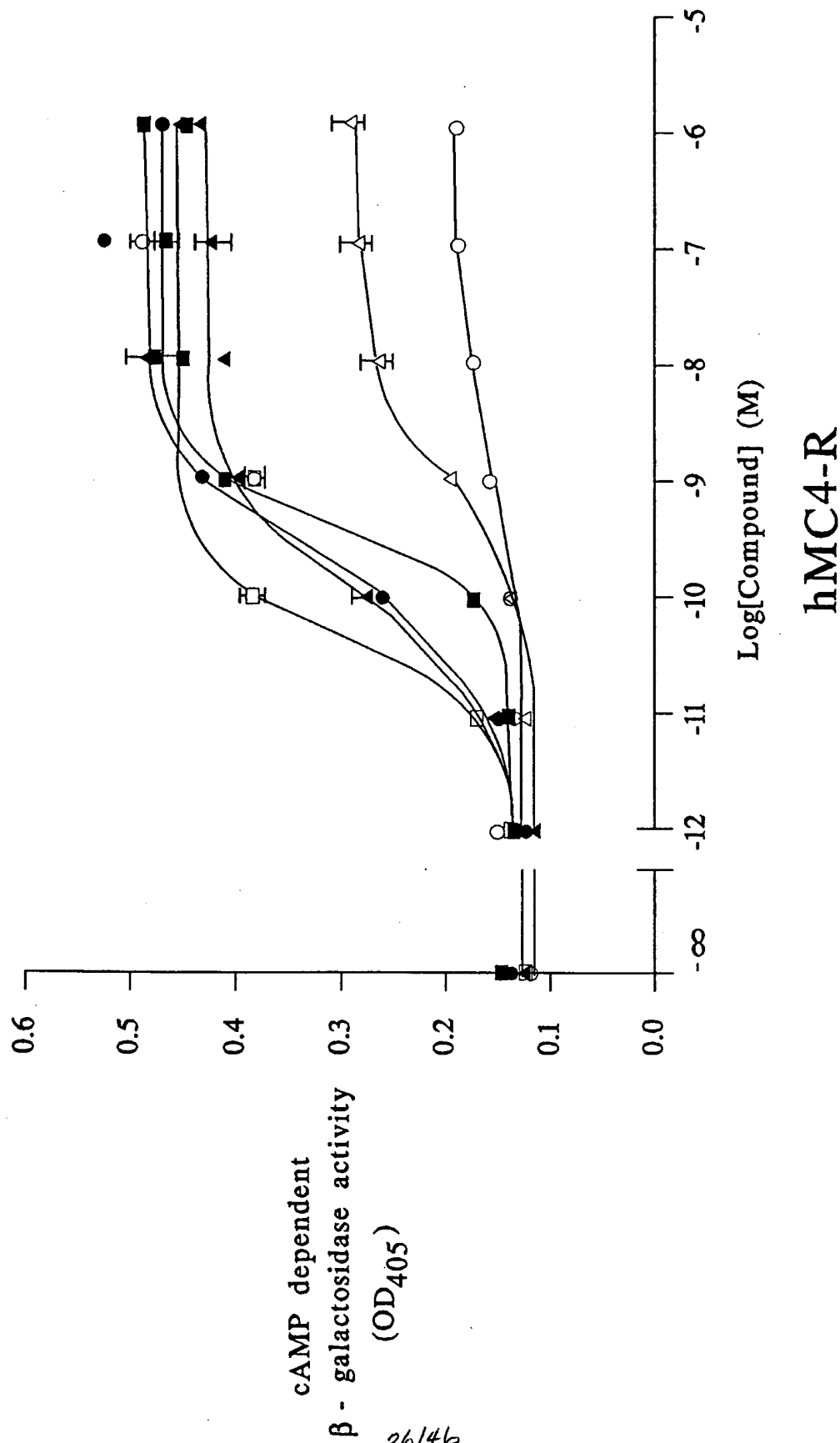
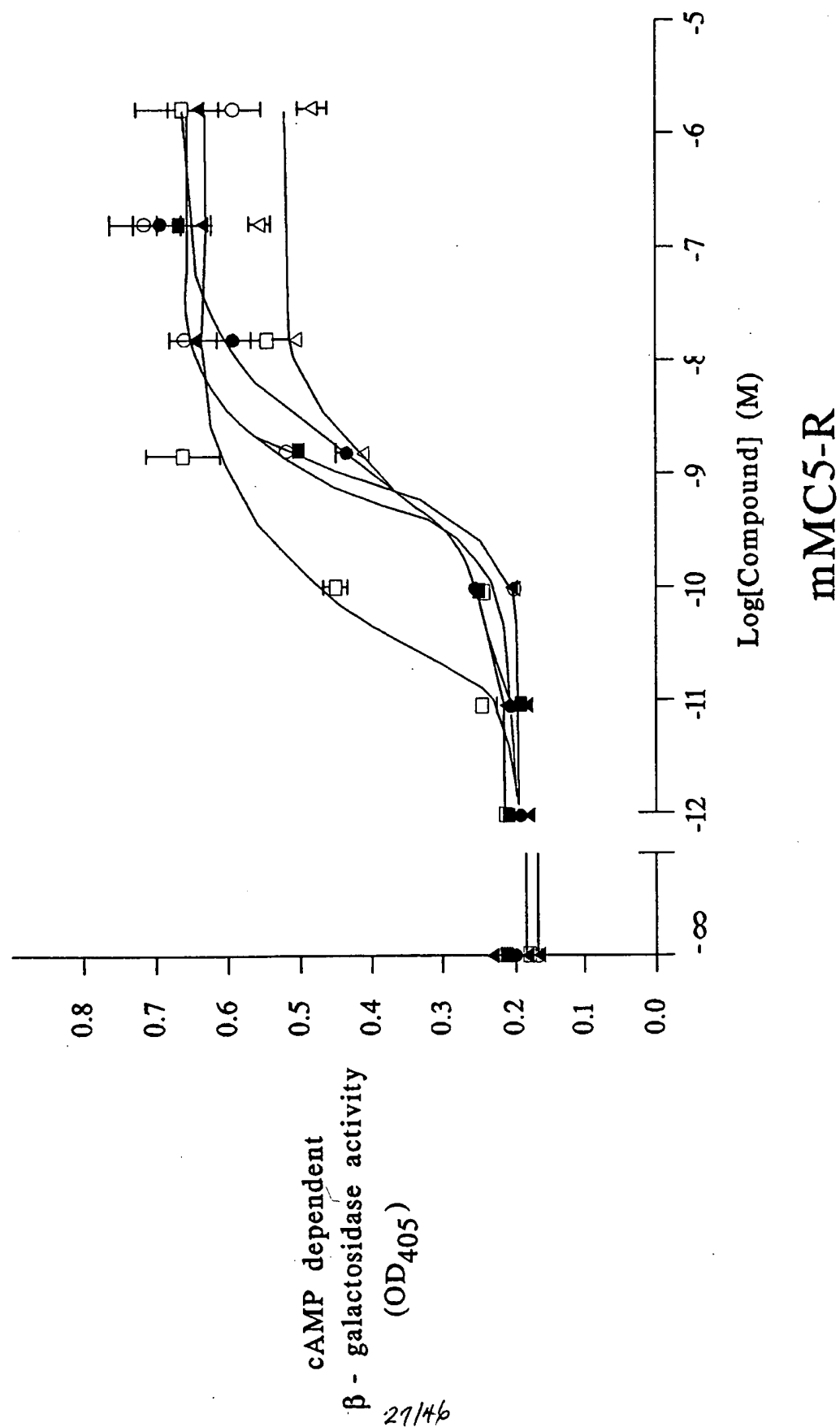
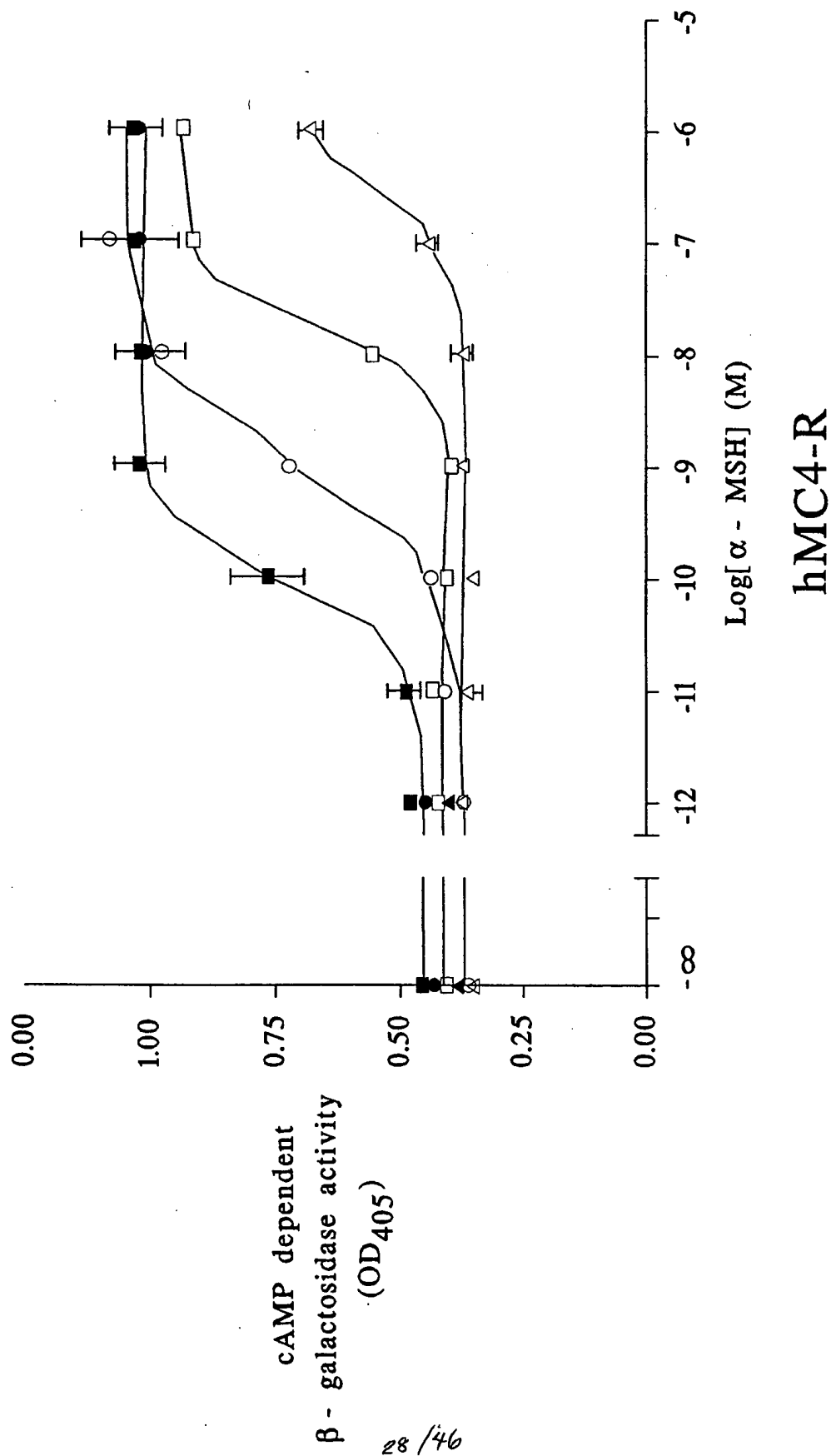
FIG. 15C

FIG. 15D

27/46

FIG. 16A

28/46



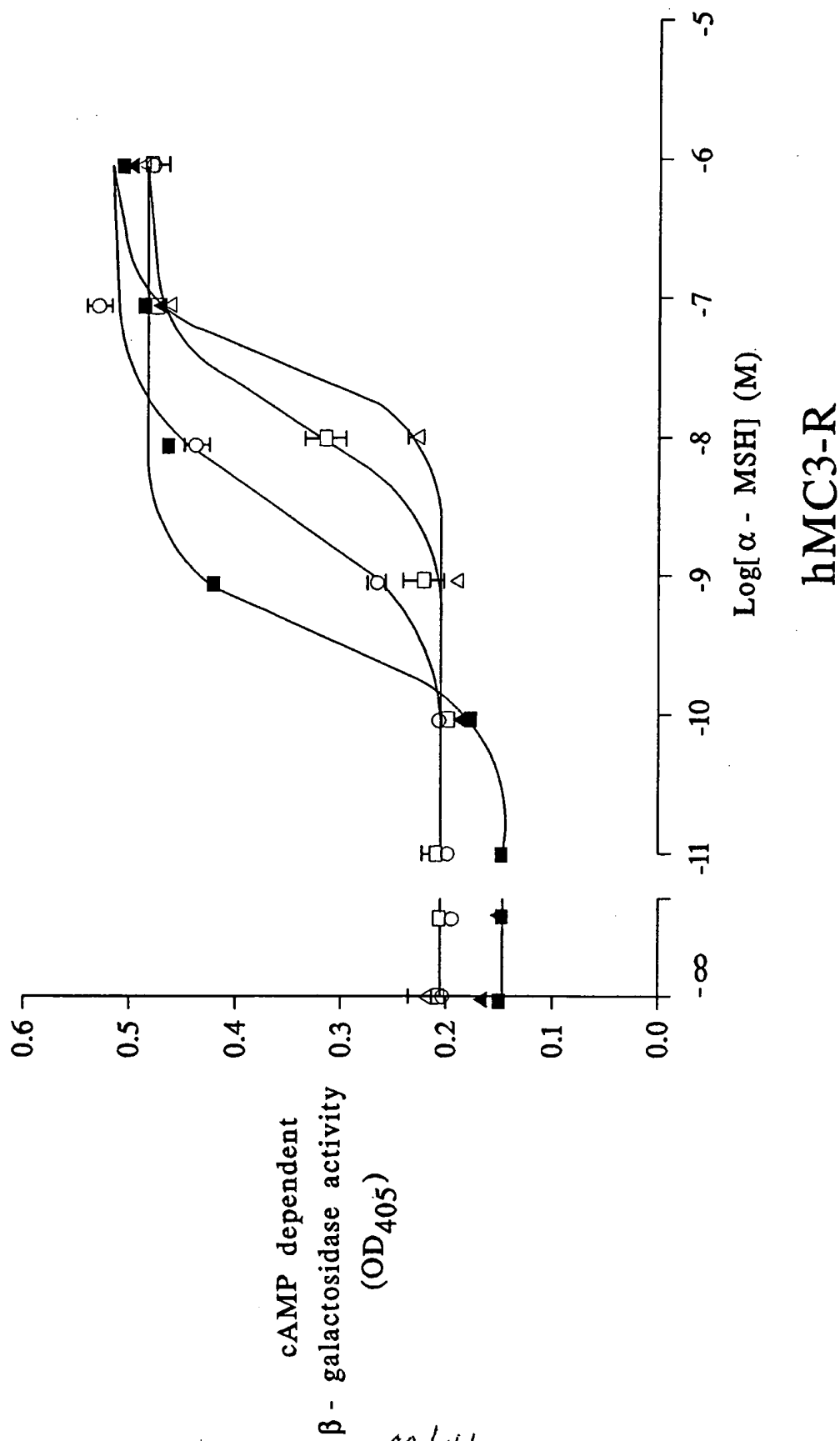
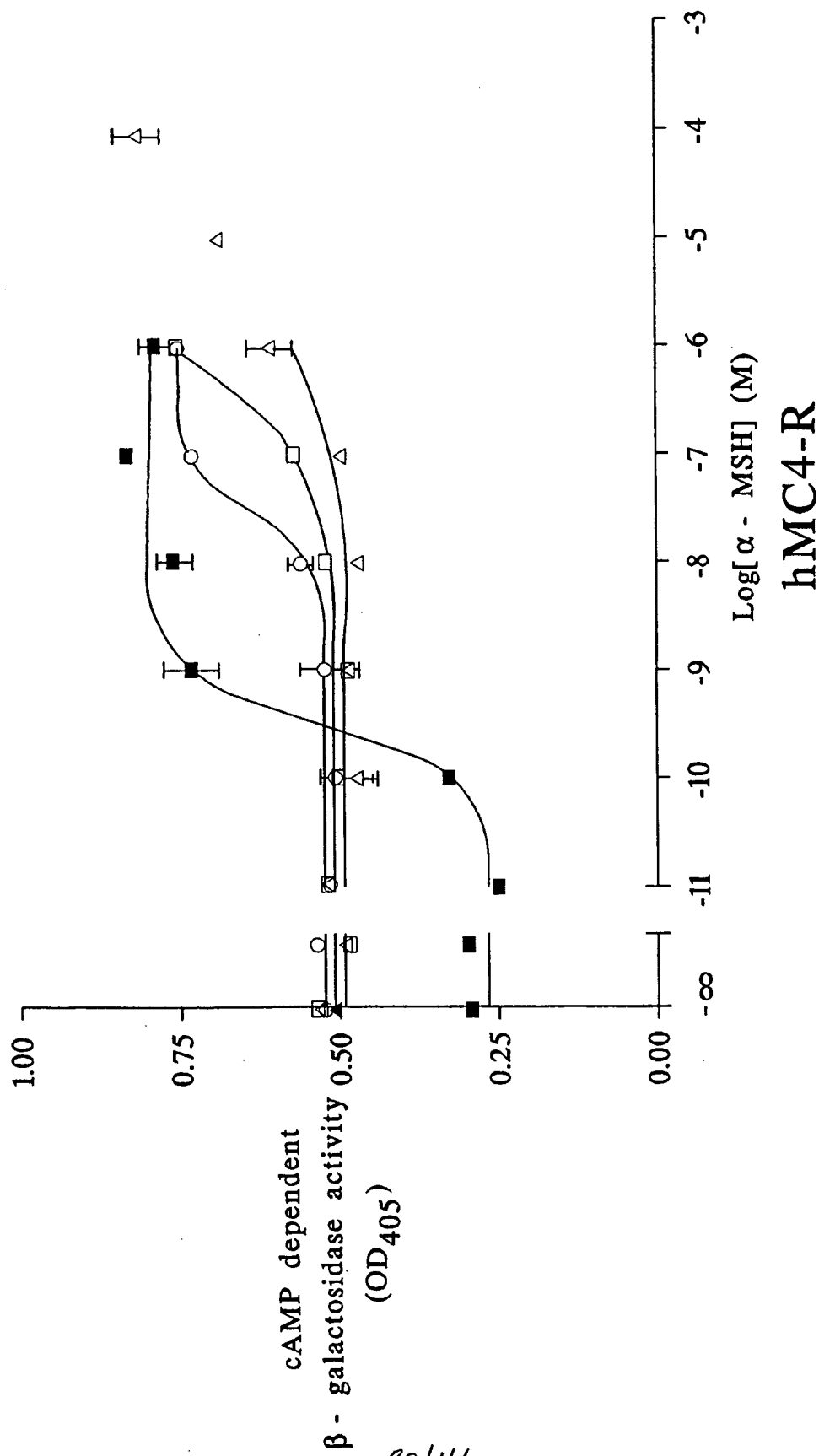
FIG. 16B

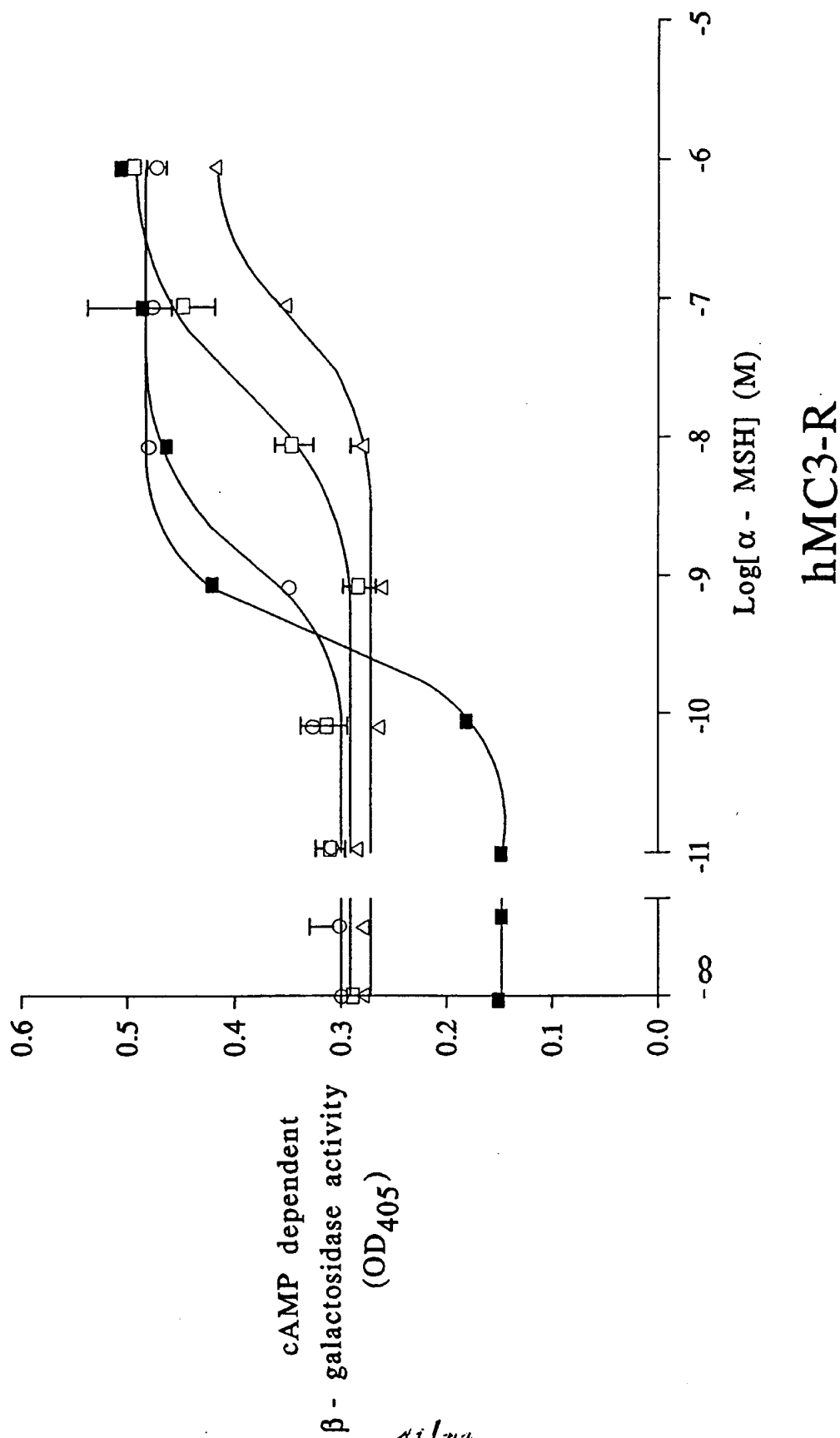
FIG. 16C



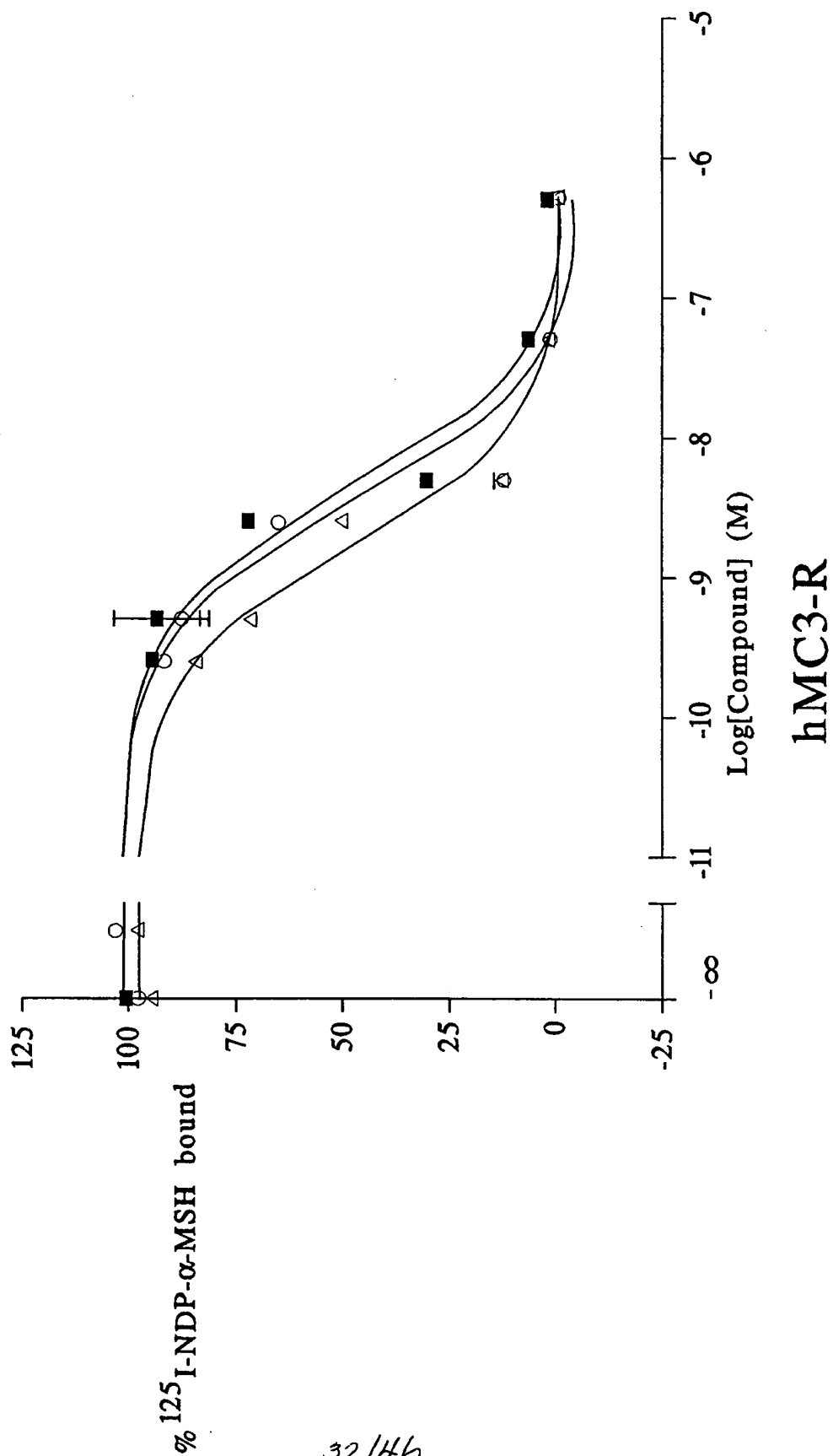
30/46

FIG. 16D

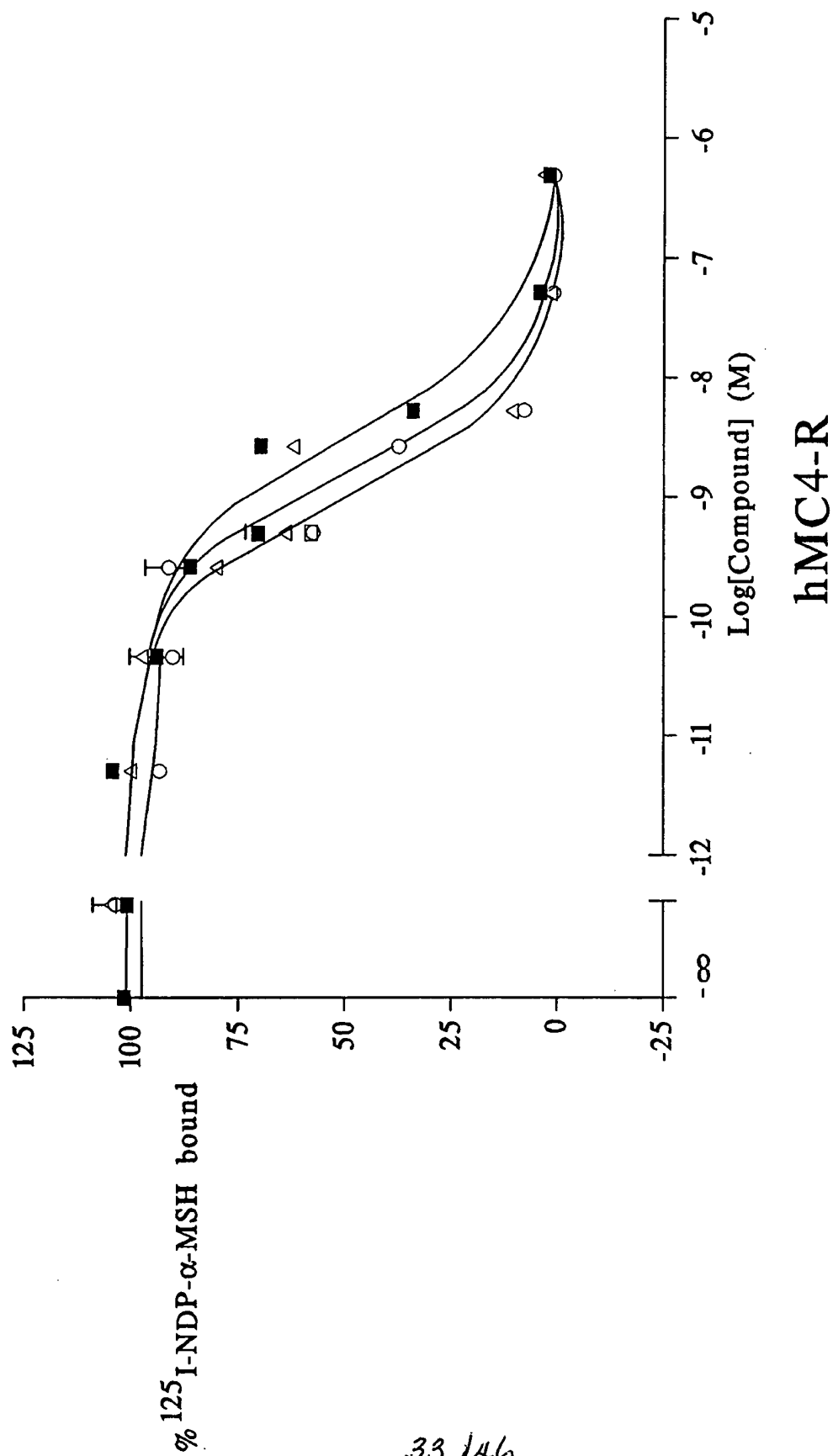
Sheet 31 of 46



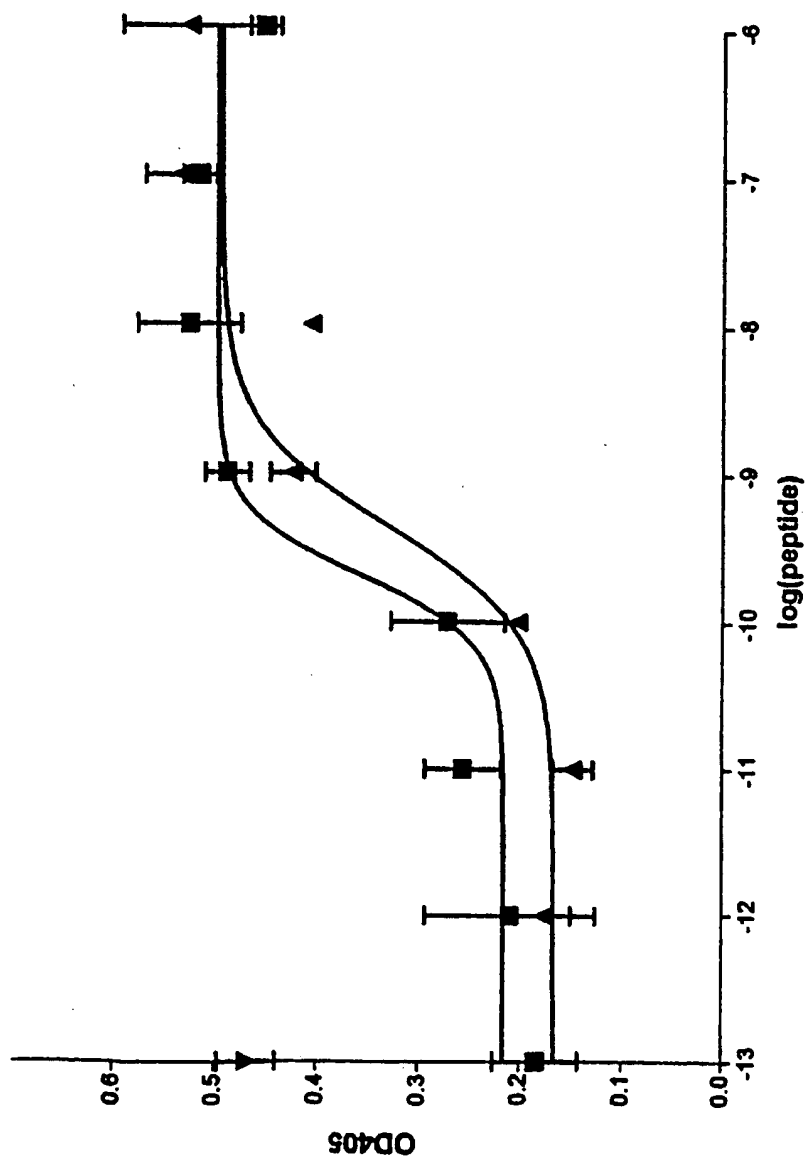
31/46

FIG. 17A

32/46

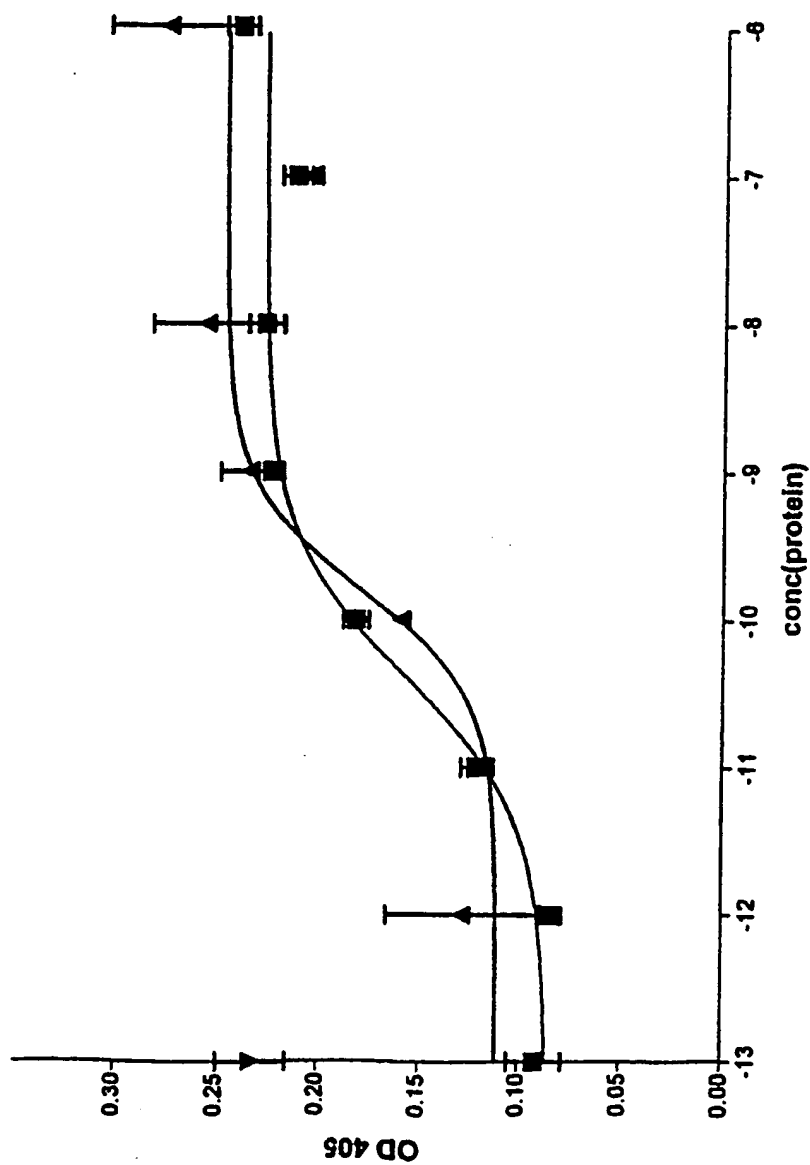
FIG. 17B

33/46

FIG. 18A

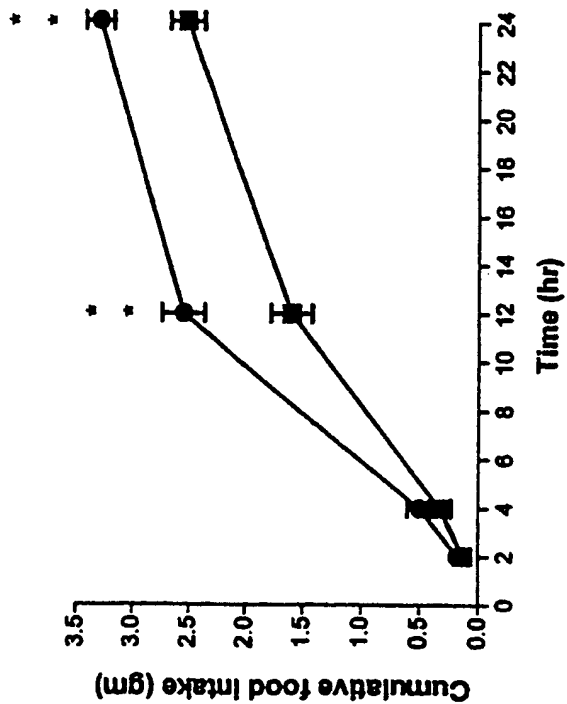
34/46

FIG. 18B



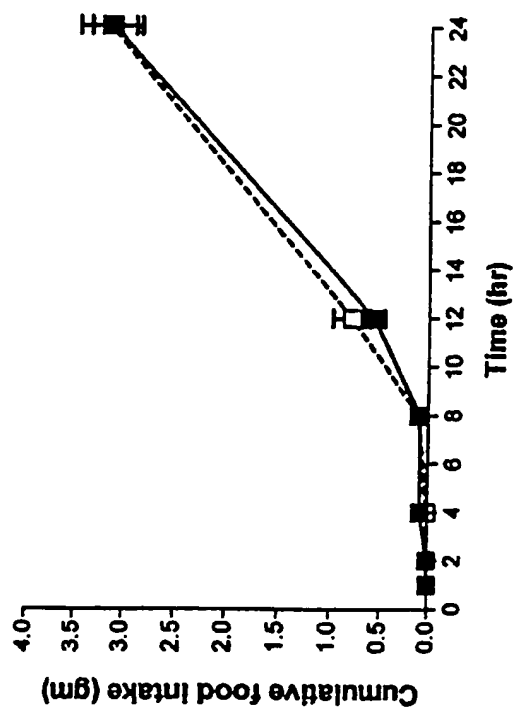
35/46

FIG. 19A



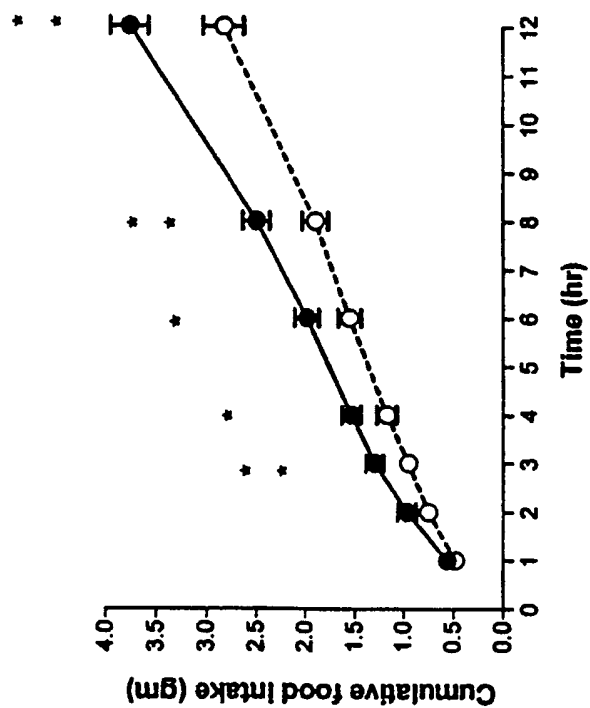
36/46



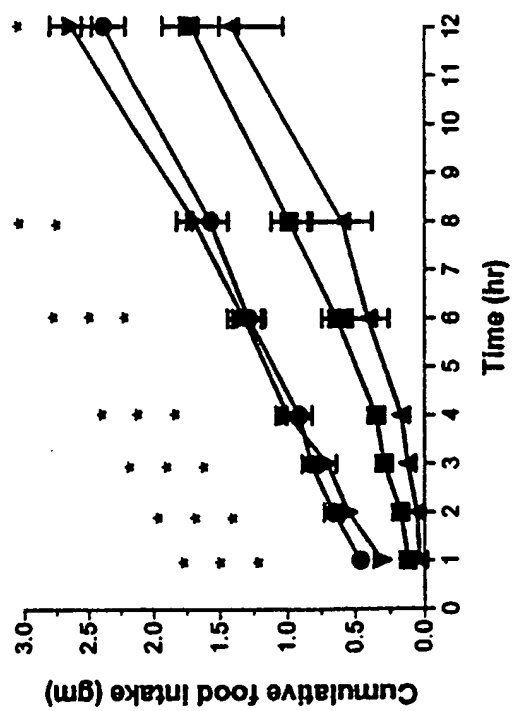
FIG. 19B

37/46

FIG. 19C

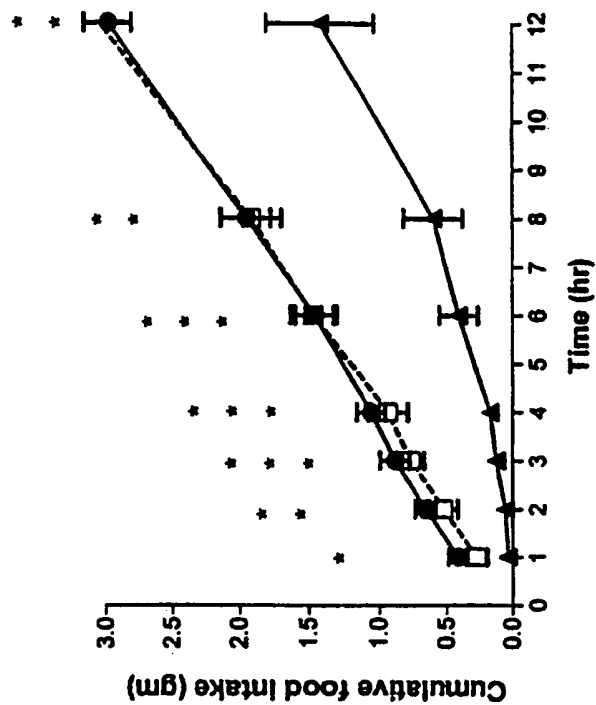


38/46

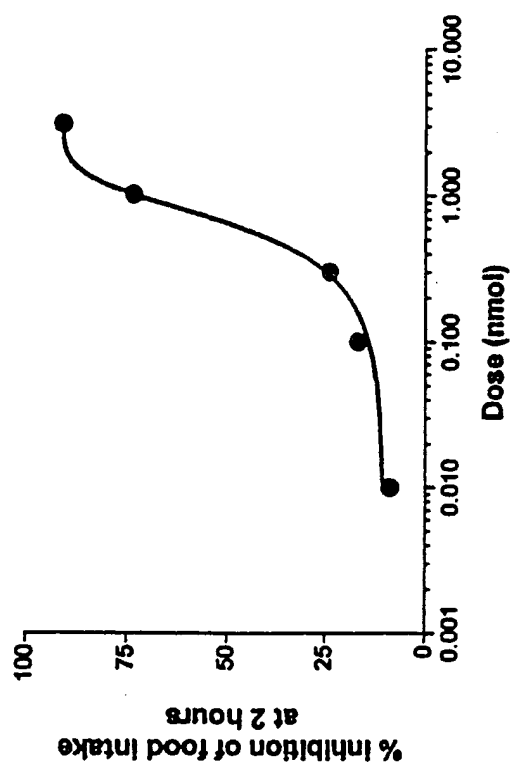
FIG. 20A

39/46

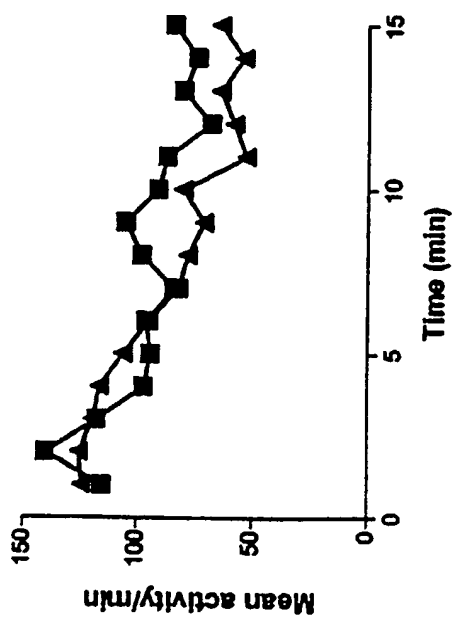
FIG. 20B



40/46

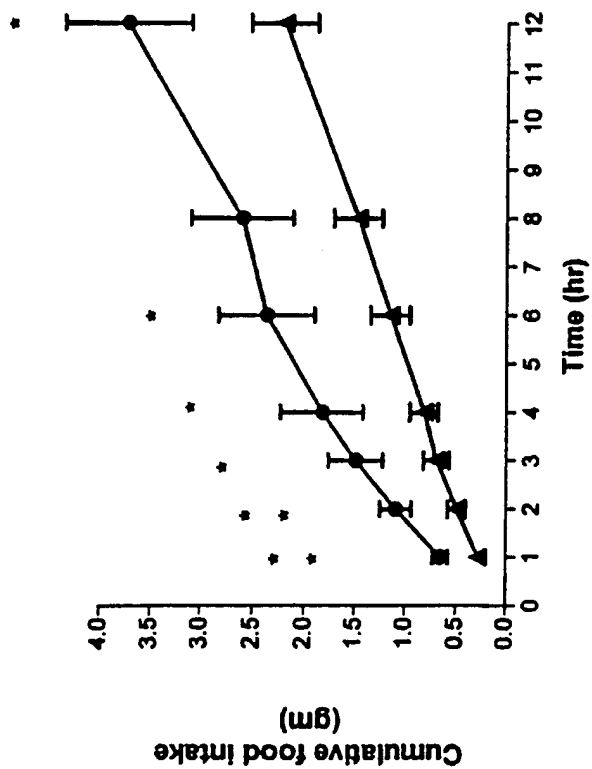
FIG. 20C

41/46

FIG. 20D

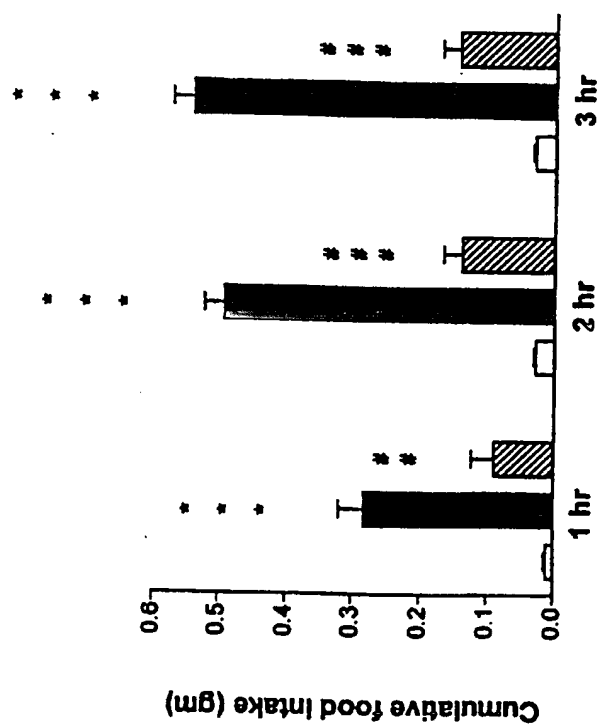
42/46

FIG. 21A



43/46

FIG. 21B



44/46



FIG. 21C

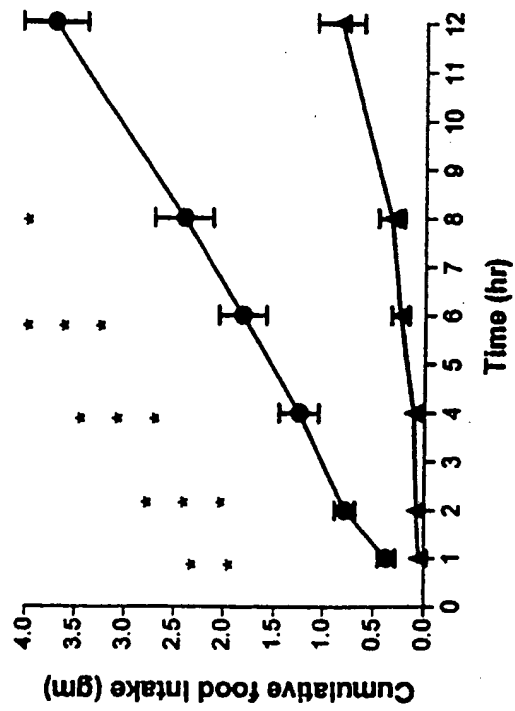
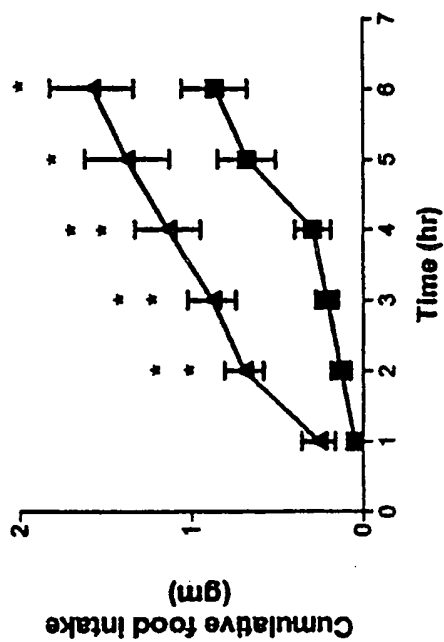


FIG. 21D



**This Page is Inserted by IFW Indexing and Scanning  
Operations and is not part of the Official Record**

**BEST AVAILABLE IMAGES**

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☐ BLACK BORDERS
- ☐ IMAGE CUT OFF AT TOP, BOTTOM OR SIDES
- ☒ FADED TEXT OR DRAWING
- ☐ BLURRED OR ILLEGIBLE TEXT OR DRAWING
- ☐ SKEWED/SLANTED IMAGES
- ☐ COLOR OR BLACK AND WHITE PHOTOGRAPHS
- ☐ GRAY SCALE DOCUMENTS
- ☐ LINES OR MARKS ON ORIGINAL DOCUMENT
- ☐ REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY
- ☐ OTHER: \_\_\_\_\_

**IMAGES ARE BEST AVAILABLE COPY.**

**As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.**

**THIS PAGE BLANK (USPTO)**